

Description

AUTHORS	Hager, P.W. and Phibbs
TITLE	Direct Submission

Hager, P.W. and Phillips, P.V. Jr
Direct Submission

as a candidate for the autosomal recessive form of Charcot-Marie-Tooth disease linked to 5q

JOURNAL
Unpublished
Reference: 1 to 910
AUTHORS
Rao H. Z., Chang H. and Francke U.
TITLE
Direct Submission
Submitted (12-JAN-1999) Department of Genetics and HMMI, Stanford
JOURNAL
University School of Medicine, B203 Beckman Center, Stanford, CA
94305, USA

FEATURES
Source
Location/Qualifiers
1:910
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Tue Jun 25 08:50:15 2002

us-09-747-514a-1.rge

Page 10

Search completed: June 23, 2002, 06:31:23
Job time: 63815 sec

GenCore version 4.5
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OM nucleic - nucleic search, using SW model

Run on: June 22, 2002, 16:27:48 ; Search time 652.13 Seconds

Title: US-09-747-514A-1

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PericL score: 20
Sequence: 1 ccgcgcctgcgcgcagcctg 20

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Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match On

Post processing: Minimum Match 10

Listing first 45 summaries

Listing first 45 summaries

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	17.4	87.0	2368	19	AAFI1865	Homo sapiens don-1
c 2	17.4	87.0	7335	12	AAFB1387	Curcuma sensu don-1
c 3	17.4	87.0	28804	17	AAI37329	Splignans biosynthesis
c 4	17.4	87.0	28804	18	AAI37329	Splignans biosynthesis
c 5	17.4	87.0	28804	20	AAI37329	Splignans biosynthesis
c 6	17.4	87.0	28804	20	AAI37329	Splignans biosynthesis
c 7	16.8	84.0	409	22	AAE65987	Novel human polyom
c 8	16.8	84.0	734	22	AAAI0140	Novel human polyom
c 9	16.8	84.0	819	19	AAI12217	Human cDNA clone of
						Malate cis-trans

[illegible]

CC A 28 kb chromosomal fragment of *Sphingomonas* strain S98 was
XX isolated on the basis of its ability to produce sphinganol.
CC The genome of the mutant *Sphingomonas* strain sphen260, it
CC contains 23-25 genes, including sps genes coding for biosynthesis of
CC the polysaccharide sphingarin. The genes coding for dtp-(L)-rhamnose
CC biosynthetis, atdib genes coding for a transport function and some
CC unidentified open translation reading frames (unf). The spsB gene
CC was identified that is believed to code for glucosyl IP-transferase
CC (AM00997), an enzyme catalysing the first step of assembly of lipo
CC sphingarin carbohydrates. DNA fragments of 586 bp can be used as
CC vectors for cloning and amplification of genes from *Sphingomonas*
CC that are hyper-producers of sphingarin.

XX Sequence 28804 BP; 4974 A; 9806 C; 9228 G; 4796 T; 0 other:

XX SQ

XX Query Match 87.0%; Score 17.4; DB 17; Length 28804;
XX Best Local Similarity 94.7%; Pctd. No. 1.2e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0

OY 1 ccgcgtcgcgcgcgaacct 19
Db 7745 ccgcgtcgcgcgcgaacct 7763
||||| |||||

RESUME 4
XX ANV92474 standard; DNA: 28804 BP.

XX AC AAm92474:
XX DT 04-FEB-1998 (first entry)
XX DX Sphingomonas genus microbe isolated DNA sequence producing sphingarin.
XX DM Sphingomonas microbe; sphingarin polysaccharide biosynthesis gene.
XX KW Sphingomonas microbe; sphingarin polysaccharide biosynthesis gene;
XX KM sphingarin S-88; spsB gene; ss.
XX XX

OS Sphingomonas sp.
XX JF09252775-A.
XX PN 30-SEP-1997.
XX PE 24-JAN-1996; 96CJP-0043977.
XX PR 16-JAN-1996; 96CJP-0004621.
XX PR 24-JUN-1995; 950S-0377440.
XX (SHIN-) SHINTSU BIO. INC.
XX (SHIE-) SHINTSU CHRM IND CO LTD.
XX WPI: 1997-530148/49.

DR Sphingarin polysaccharide biosynthesis gene from *Sphingomonas* microbe
PT - can be introduced into *Sphingomonas* host cells to increase
PT sphingarin production
PS Claim 74; Page 34-43; 55pp; Japanese.

XX The present sequence represents a new DNA sequence which has been
XX isolated from a sphingarin polysaccharide-producing microbe of the
XX genus *Sphingomonas*. When recombined in a *Sphingomonas* host, the
XX presence of several copies of the sphingarin polysaccharide biosynthesis
XX genes has been developed for producing a *Sphingomonas* microbe with
XX enhanced sphingarin polysaccharide expression, by transforming the cell
XX with the sphingarin polysaccharide biosynthesis gene. The method can
XX produce sphingarin in large quantities.

XX Sequence 28804 BP; 4974 A; 9804 C; 9230 G; 4796 T; 0 other:

Claim 32: Page 56-70; 105pp: English.

Query Match 87.0%; Score 17.4; DB 18; Length 28804;
 Best Local Similarity 94.7%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ccgcgcgcgcgcgcgcgcct 19
 ||||||| ||||||| |||||||
 Db 7745 ccgcgcgcgcgcgcgcgcct 7763

RESULT 5

AAV9812 standard; DNA; 28804 BP.

AAV9812;

14-JUN-1999 (first entry)

Sphingomonas S88 sps gene cluster.

Xanthan gum: gum; exopolysaccharide; gum gene cluster;
 recombination; Xanthomonas; Sphingomonas; sphingon S88; sugar;

substrate; lactose; sucrose; starch; ss.

Sphingomonas sp. S88.

MO9856942-A1.

17-DEC-1998.

12-JUN-1998; 98MO-US12322.

12-JUN-1998; 98US-0096642.

12-JUN-1998; 97US-0046423.

11-JUN-1998; 98US-0096667.

(SHIN-) SHINETSU BIO INC.

(SITE) SHINETSU CHEM CO LTD.

Armentrout RM, Mikolajczak M, Pollock TJ, Thorne L;

Yamazaki M;

WPI; 1999-080915/07.

Production of exopolysaccharide, e.g. xanthan gum by a Sphingomonas

species bacterium - containing the gum-M genes of X. campestris,

and using lactose as a C source

Example 1: Page 36-46; 50pp; English.

Xanthan gum is an exopolysaccharide produced by Xanthomonas species

and encoded by the gum gene cluster. The gum gene cluster of

Xanthomonas campestris can be inserted into a Sphingomonas species

of bacterium. The gum gene cluster is inserted into the Sphingomonas

species. The gum gene cluster represents an exopolysaccharide.

Sphingomonas S88. The new novel, lactose-utilizing Sphingomonas

by-product xanthan gum from sugar substrates 1.e. the cheese-making

production of Xanthan gum. Use of the Sphingomonas species in its

medium into which the xanthan gum is secreted.

Sequence 28804 BP; 4974 A; 9804 C; 9230 G; 4796 T; 0 other;

Query Match 87.0%; Score 17.4; DB 20; Length 28804;
 Best Local Similarity 94.7%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ccgcgcgcgcgcgcgcgcct 19
 ||||||| ||||||| |||||||
 Db 7745 ccgcgcgcgcgcgcgcgcct 7763

RESULT 6

AAV81474 standard; DNA; 28804 BP.

AAV81474;

16-MAR-1999 (first entry)

Chromosomal fragment of Sphingomonas strain 88 genome.

Chromosome: sphingon; bacterium; polysaccharide; polymer; additive; food;

glycosyl-C55-isoprenylphosphate transferase; textile; cosmetic; paper;

paint; cement; viscosity; adhesive; petroleum; chemical; ds.

Sphingomonas sp.

Key Location/Qualifiers

CDS 28804..28818

/product="spsb protein"

US5854034-A.

23-DEC-1998.

24-JAN-1996; 96US-0592874.

24-JAN-1996; 96US-0592874.

24-JAN-1995; 95US-0377440.

(SHIN-) SHIN-ETSU CO INC.

(SITE) SHINETSU CHEM CO LTD.

Armentrout RM, Mikolajczak M, Pollock TJ, Thorne L;

Yamazaki M;

WPI; 1999-054309/08.

Production of sphingon polysaccharide products - by introducing DNA

from sphingon-producing Sphingomonas species in multiple copies into

recipient Sphingomonas sp.

Example 16; Fig 14A-K; 66pp; English.

This sequence represents a chromosomal fragment of the Sphingomonas sp.

and encoded by the gum gene cluster. The gum gene cluster can be

used to increase production of sphingon polysaccharides in other

microorganisms, especially other Sphingomonas strains. The DNA

transferred to other strains includes the spsB gene which encodes a

glycosyl-C55-isoprenylphosphate (glycosyl-IP) transferase. The sphingans

are useful as specialty polymers and as additives in textile

applications, foods, cosmetics, paper, paint, cements, e.g. as viscosity

additives to petroleum products and specialty chemicals.

Sequence 28804 BP; 4974 A; 9804 C; 9230 G; 4796 T; 0 other;

Query Match 87.0%; Score 17.4; DB 20; Length 28804;
 Best Local Similarity 94.7%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ccgcgcgcgcgcgcgcgcct 19
 ||||||| ||||||| |||||||
 Db 7745 ccgcgcgcgcgcgcgcgcct 7763

RESULT 7
 AAV5897/C
 ID AAV5897 standard; cDNA; 409 BP.

XX XX AAF5897;
 XX XX 09-APR-2001 (first entry)
 XX XX
 DE Novel human polynucleotide, SEQ ID NO: 1653.
 XX
 XX Human: cytostatic; gene therapy: colon cancer; prostate cancer;
 XX breast cancer; lung cancer; cancer detection; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200102568-A2.
 XX
 PD 11-JAN-2001.
 XX
 PR 30-JUN-2000; 2000MO-US18374.
 XX
 PR 02-JUL-1999; 99US-0142310.
 XX
 PR 02-JUL-1999; 99US-0142311.
 XX
 PA (CHIE) CHIRON CORP.
 XX
 PA (HIS-) HISQ INC.
 XX
 PI Williams LR, Escobedo J, Innis MA, Garcia PO, Klinger J, Kassam A;
 PI Reinhard C, Randozo F, Kennedy GC, Pot D, Lamson G, Drmanac R;
 PI Cirenjakov R, Drmanac S, Dickson M, Labat I, Leshowitz D;
 PI Kita D, Garcia V, Jones LW, Strache-Grain B;
 XX
 NM WPI: 2001-091805/10.
 XX
 PT Library of polynucleotides for diagnosing a cancerous state of a
 PT mammalian cell and detecting cancer, particularly of the colon or
 PT prostate, comprises 3351 human polynucleotide sequences -
 XX
 PS Claim 9; Page 781; 1046pp; English.
 XX
 XX The present sequence is one of 3351 sequences in a library of human
 XX polynucleotides. The library is used to detect differentially expressed
 XX genes correlated with a cancerous state of a mammalian cell and can
 XX detect colon, prostate, breast and lung cancer. The library can be used
 XX to produce probes for detection of mRNA and to produce additional copies
 XX of the polynucleotides. The probes can be used for chromosome mapping of
 XX the polynucleotide and for detection of transcription levels of genes
 XX or antisense oligonucleotides as genetic or biochemical markers (e.g. in
 XX blood or tissues) that will detect the earliest changes along the 9. In
 XX carcinogenesis pathway and/or monitor the efficacy of therapies and
 XX preventive interventions. The polynucleotides, polypeptides and
 XX antibodies against them can be used in pharmaceutical compositions to
 XX treat the cancers and proliferative disorders such as neoplasia,
 XX dysplasia and hyperplasia.
 XX
 SO Sequence 409 BP; 108 A; 80 C; 122 G; 100 T; 0 other;

Query Match 84.0%; Score 16.8; DB 22; Length 409;
 Best Local Similarity 90.0%; Pred. No. 3.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

0Y 1 CCGCGCTCGCGCGCGCTG 20
 ||||||| 1111111
 DB 24 CCGCGCTCGCGCTGACGCGT 5

RESULT 8
 AAH05140/1
 AAH05140 standard; cDNA; 734 BP.
 XX
 XX AAH05140;
 XX
 DT 26-JUN-2001 (first entry)

DE Human cDNA clone (5'-primer) SEQ ID NO:1975.
 XX
 XX Human: primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 XX EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-0116126.
 XX
 PR 29-JUL-1989; 89JP-0246935.
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 PR 29-JUL-1989; 89JP-0246935.
 XX
 PR 11-MAY-2000; 2000JP-0118776.
 XX
 PR 02-MAY-2000; 2000JP-0183767.
 XX
 PR 09-JUN-2000; 2000JP-0241899.
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 PA (HELI-) HELIX RES INST.
 XX
 PI Oka T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 NM WPI: 2001-318749/34.
 XX
 DR
 XX
 PT primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 1; SEQ ID 1975; 2537pp + CD ROW; English.
 XX
 XX The present invention describes primer sets for synthesizing 5602
 XX full-length cDNAs defined in the specification, where a primer set
 XX comprises: (a) an oligo of primer, and (b) an oligo of complementary
 XX strand of the same length as the primer, and a method of synthesizing
 XX the 5602 full-length cDNAs defined in the specification, where the
 XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 XX of an oligonucleotide comprising a sequence complementary to the
 XX complementary strand of a polynucleotide which comprises a 5'-end
 XX sequence and an oligonucleotide comprising a sequence complementary to a
 XX polynucleotide which comprises a 3'-end sequence, and the combination of
 XX the oligonucleotide sequence/3'-end sequence is selected from those defined in
 XX the specification. The primer sets can be used in antisense therapy and
 XX in gene therapy. The primers are useful for synthesizing polynucleotides,
 XX particularly full-length cDNAs. The primers are also useful for the
 XX detection and/or diagnosis of the abnormality of the proteins encoded by
 XX the full-length cDNAs. The primers allow obtaining 5602 full-length
 XX cDNAs easily. AAH1975 and present human cDNA sequences; AAH92446 to
 XX AAH9883 represent human amino acid sequences; and AAH15629 to AAH16322
 XX represent oligonucleotides, all of which are used in the exemplification
 XX of the present invention.
 XX
 SO Sequence 734 BP; 205 A; 139 C; 183 G; 194 T; 13 other;

Query Match 84.0%; Score 16.8; DB 22; Length 734;
 Best Local Similarity 90.0%; Pred. No. 3.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

0Y 1 CCGCTCGCGCGCGCGCTG 20
 ||||||| 1111111
 DB 64 CCGCGCTCGCGCTGACGCGT 45

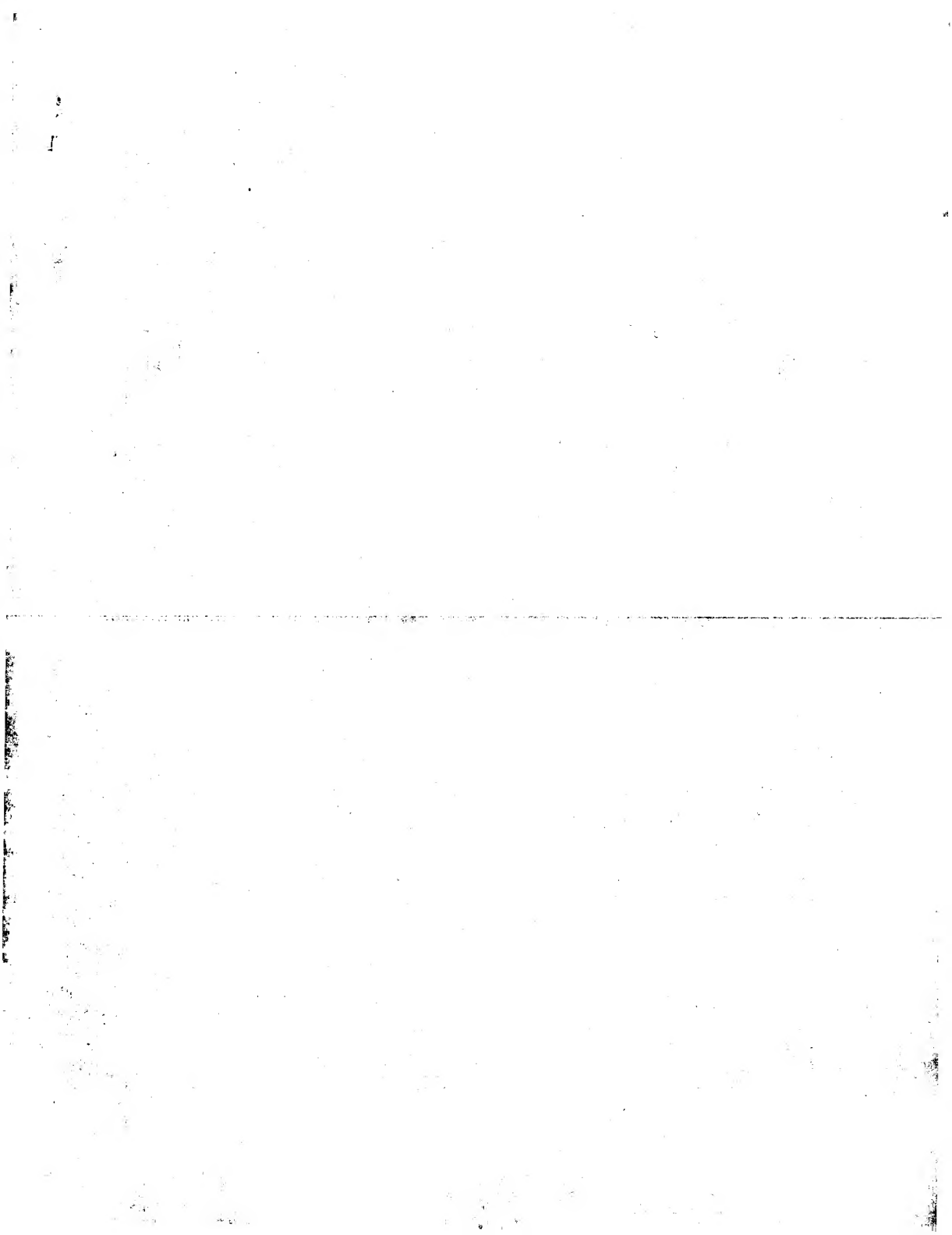
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 ID AAH12277 standard; DNA; 819 BP.
 XX
 XX AAH12277;
 XX

DT	12-MAY-1998 (first entry)
DE	Maleate cis-trans isomerase encoding DNA.
XE	
XX	Maleate cis-trans isomerase; maleic acid; fumaric acid; antioxidant;
KM	baking powder; fruit juice; tartaric acid; citric acid; DS.
KS	
OS	Arthrobaacter globiformis.
PN	
PP	JPI003J181-A.
PD	10-FEB-1998.
PE	24-JUL-1996; 96JP-0194961.
PF	24-JUL-1996; 96JP-0194961.
PA	(MITU) MITSUBISHI CHEM CORP.
DR	WPI: 1998-172098/16.
DR	P-PDSB; AANA4186.
PT	Maleate cis-trans isomerase from Arthrobaacter globiformis IAM 12102
PT	of maleic acid
PT	The efficient production of fumaric acid by isomerisation
PS	Claim 1: Page 10-11: 14pp; Japanese.
CC	
CC	The present sequence encodes maleate cis-trans isomerase, isolated
CC	from Arthrobaacter globiformis IAM 12102. Maleate cis-trans isomerase
CC	is an enzyme or catalytic agent which converts maleic acid to fumaric acid.
CC	The enzyme or catalyst converting maleic acid to produce fumaric acid,
CC	aqueous solution containing maleic acid to produce fumaric acid,
CC	Fumaric acid is useful as a substitute for tartaric acid in beverages
CC	and baking powders and as a replacement for citric acid in fruit
CC	drinks. Fumaric acid is also used as an antioxidant.
XX	
XX	Sequence 819 BP; 155 A; 299 C; 250 G; 115 T; 0 other:
Db	
QY	1 ccgcgctcgagccgcgaacctg 20 cgcgcctgcgcgcgcgcgcgc 600
RESULT 10	
ID	AAN46831/C
AAH46831	standard; cDNA: 1877 BP.
XX	
XX	AAN46831L
XX	
DT	25-SEP-2001 (first entry)
DE	Human immunoglobulin domain-containing polypeptide encoding cDNA.
KM	
KM	immunoglobulin domain-containing polypeptide; secreted protein; human;
KM	cytotoxic; immunosuppressive; antiinflammatory; antipneumtic; vaccine;
KM	necrotic; osteoporosis; antiproliferic; antibacterial; fungicide;
KM	antitumor; antidiabetic; antiparasitoidan; antiallergic;
KM	antihemostatic; dermatological; cerebroprotective; antidiabetic;
XX	hemostatic; gene therapy; ss.
XX	
OS	Home sapiens.

	Ft	Key	Location/Qualifiers			
	Pt	CDS	/tag= "a 54...920			
	Ft	exon	/note= "contains introns"			
	Ft	intron	/tag= "b 54...363 57...821 56...621 c /tag= "c number= "1" 622..917 /tag= "d /number= "2"			
Df	Xx		W020015534-?2.			
Pd	Xx		02-AUG-2001.			
Pf	Xx		25-JAN-2001; 2001WO-US02461.			
Pg	Xx		25-JAN-2000; 2000US-0491404. 03-FEB-2000; 2000US-0496914. Pz	03-FEB-2000; 2000US-0496914. Pr	04-OCT-2000; 2000US-0680845; Pa	(HYSE-) HYSEQ INC.
Pi	Xx		Boyle BJ, Artztubun MC, Tang YT, Liu C, Dmanac RA;			
Pj	Xx		wpi: 2001-476187/51.			
Pk	Xx		p-psdb: AA854820.			
Pn	Xx		Noel immunoglobulin domain-containing polypeptides and poly nucleotides useful for diagnosis, prevention, treatment of cancer, rheumatoid disorders, immunological diseases, such as psoriasis, rheumatoid arthritis -			
Po	Xx		claim 1; Page 125-127; 132pp; English.			
Pq	Xx		The invention provides novel human secreted immunoglobulin domain-			
Ps	Xx		-containing polypeptides (I) and polynucleotides (II) encoding them.			
Pt	Xx		The polypeptide exhibits cytokine, cell proliferation or cell differentiation, stem cell growth factor activity and activin or inhibin related activities, chemoreactive or chemokinetic activities, (1) is useful for engineering healthy damaged or diseased tissues, transplantation,			
Pv	Xx		AH46827 for a detailed description of the uses and diseases that can be treated by using the polypeptides of the invention). The present sequence represents a immunoglobulin domain-containing polypeptide encoding cDNA.			
S0	Xx		Sequence 1877 BP; 518 A; 398 G; 471 G; 489 T; 1 other;			
Oy		Query Match	Score 16.8; DB 22; Length 1877;			
Bz		Best Local Similarity	94.0%; Pred. No. 3,3e+02;			
Matches	18:	Conservative	0; Mismatches 2; Indels 0; Caps 0			
Oy		1 ccgcggctcgccgccagctcg 20				
Df		1058 ccgcggcccccgcgcacactg 1039				
Rsgult_11	ID	AAAS84820/c				
AC		AAAS84820 standard; cDNA: 2934 BP.				
XX		AAAS84820.				
XX		13-FEB-2002 (first entry)				
XX		DNA encoding novel human diagnostic protein #20624.				
Hmnn:		chromosome mapping; gene mapping; gene therapy; forensic;				

CC Identify antibodies or proteins that block the acrosome reaction and
CC inhibit sperm-egg fusion. The acrosome reaction is the process by which
CC sperm release enzymes that allow them to penetrate the zona of zona
CC pellucida. Molecules that enhance the efficacy of the acrosome reaction
CC protein can be used to increase fertility and those blocking its
CC action can be used as contraceptives. DNA encoding PKDREJ can be used in
CC gene therapy and also as primer or probe for identifying sequences that
CC encode mutant forms of acrosome reaction protein.
XX
SQ Sequence 7686 BP; 1952 A; 1827 C; 1809 G; 2098 T; 0 other:
Query Match 84.0%; Score 16.8; DB 21; Length 7686;
Best Local Similarity 90.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 ccgagctcgcgcgagcctg 20
Db 190 cccgcctcgcgcgcgagcctg 171

Search completed: June 23, 2002, 14:59:54
Job time: 81126 sec



Query Match 87.0% Score 17.4; DB 3; Length 2268;
 Best Local Similarity 94.7% Pred. No. 43;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 2 cgcgcctgcgcgcgcgcctg 20
 Db 1532 cccctcgcgcgcgcgcctg 1550

RESULT 2

US-09-398-496-31
 ; Sequence 31, Application US/09398496
 ; Patent No. 6133423
 ; GENERAL INFORMATION:
 ; APPLICANT: Gearling, David P.
 ; TITLE OF INVENTION: BAREFIELD, Samantha J.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: IBM Compatible
 ; SOFTWARE: FASTSEQ Version 2.0
 ; CURRENT FILING DATE: 2001-03-27
 ; APPLICATION NUMBER: US/09/398,496
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/753,007
 ; FILING DATE: 19-NOV-1996
 ; PRIORITY NUMBER: 08/699,581
 ; FILING DATE: 19-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Passero, J. Peter
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 07334/022001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-8967
 ; TELEFAX: 617-542-8906
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2268 base pairs
 ; TYPE: nucleic acid
 ; STRATEGY: full-length
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 69...2009
 ; OTHER INFORMATION:
 ; US-09-398-496-31

Query Match 87.0% Score 17.4; DB 3; Length 2268;
 Best Local Similarity 94.7% Pred. No. 43;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 cgcgcctgcgcgcgcgcctg 20

Db 1532 cccctcgcgcgcgcgcctg 1550

RESULT 3

US-09-817-180-3/c
 ; Sequence 3, Application US/09817180
 ; Patent No. 6340774
 ; GENERAL INFORMATION:
 ; APPLICANT: GAN, Melvin et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: C1001183
 ; PRIORITY NUMBER: US/09/817,180
 ; CURRENT FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 15297
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-817-180-3

Query Match 87.0% Score 17.4; DB 4; Length 15297;
 Best Local Similarity 94.7% Pred. No. 35;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 cgcgcctgcgcgcgcgcctg 19

Db 1873 cccctcgcgcgcgcgcctg 1855

RESULT 4

US-09-773-816-1
 ; Sequence 1, Application US/09773816
 ; Patent No. 6340774
 ; GENERAL INFORMATION:
 ; APPLICANT: Stanford University
 ; APPLICANT: Knosla, Chaitan
 ; TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR
 ; TITLE OF INVENTION: ANTAGONISTS
 ; FILE REFERENCE: C1001183
 ; PRIORITY NUMBER: US/09/773,816
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/243,458
 ; PRIOR FILING DATE: 2000-10-25
 ; PRIOR APPLICATION NUMBER: US 60/179,305
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ NOS:
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 23673
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc-feature
 ; LOCATION: (1) (23623)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-773-816-1

Query Match 87.0% Score 17.4; DB 4; Length 23673;
 Best Local Similarity 94.7% Pred. No. 33;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 cgcgcctgcgcgcgcgcctg 20

Db 3324 cgcgcctgcgcgcgcgcctg 3342

RESULT 5

US-08-592-874-1
 ; Sequence 1, Application US/08592874
 ; Patent No. 5854034
 ; GENERAL INFORMATION:
 ; APPLICANT: POLLOCK, THOMAS J.

```

APPLICANT: YAMAZAKI, MOTOHIDE
APPLICANT: THORNE, LINDA
APPLICANT: MIKOLAJCZAK, MARCIA
APPLICANT: ARMENTROUT, RICHARD W.
TITLE OF INVENTION: DNA SEQUENCES AND METHODS FOR INCREASING
TITLE OF INVENTION: POLYMERASE ACTIVITY IN BACTERIAL PRODUCTION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: JULES E. GOLDBERG
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: US
ZID: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/592.874
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/377,440
FILING DATE: 24-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
FIRM: GOLDBERG, JULES E. & ASSOCIATES
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-866-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28804 base pairs
NATURE: nucleic acid
STRANDS: 1 strand
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FRAGMENT TYPE: N-terminal
US-08-592-874-1

Query Match
87.0%: Score 17.4; DB 2; Length 28804;
Best Local Similarity 94.7%: Pred. No. 33;
Matches 18: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cccgcctcgcgcgcgcgcct 19
DB 7745 cccgcctcgcgcgcgcgcct 7763

RESULT 6
US-09-096-942-2
Sequence 2, Application US/09096942
GENERAL INFORMATION:
APPLICANT: POLLOCK, THOMAS J
APPLICANT: MIKOLAJCZAK, MARCIA
APPLICANT: ARMENTROUT, RICHARD W
APPLICANT: THORNE, LINDA
APPLICANT: ARMENTROUT, RICHARD W
TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria
FILE REFERENCE: seq list for appl filed from pro. appl
CURRENT APPLICATION NUMBER: US/09/096.942
FILING DATE: 1998-06-12
EXAMINER FILING DATE: 1997-06-12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 28804

```

```

TYPE: DNA
ORGANISM: Sphingomonas sp. S88
US-09-096-942-2

Query Match
87.0%: Score 17.4; DB 3; Length 28804;
Best Local Similarity 94.7%: Pred. No. 33;
Matches 18: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cccgcctcgcgcgcgcgcct 19
DB 7745 cccgcctcgcgcgcgcgcct 7763

RESULT 7
US-09-096-867-2
Sequence 2, Application US/09096867
GENERAL INFORMATION:
APPLICANT: POLLOCK, THOMAS J
APPLICANT: MIKOLAJCZAK, MARCIA
APPLICANT: ARMENTROUT, RICHARD W
APPLICANT: THORNE, LINDA
APPLICANT: ARMENTROUT, RICHARD W
TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria
FILE REFERENCE: seq list for appl filed from pro. appl
CURRENT APPLICATION NUMBER: US/09/096.867
FILING DATE: 1998-06-12
EXAMINER FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 28804
TYPE: DNA
ORGANISM: Sphingomonas sp. S88
US-09-096-867-2

Query Match
87.0%: Score 17.4; DB 3; Length 28804;
Best Local Similarity 94.7%: Pred. No. 33;
Matches 18: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cccgcctcgcgcgcgcgcct 19
DB 7745 cccgcctcgcgcgcgcgcct 7763

RESULT 8
US-09-160-483-2/c
Sequence 2, Application US/09160483A
GENERAL INFORMATION:
APPLICANT: MARCU, KENNETH B.
TITLE OF INVENTION: A BIOLOGICALLY ACTIVE ALTERNATIVE FORM OF THE IKK
FILE REFERENCE: Docket No. 608732; 178-255
CURRENT APPLICATION NUMBER: US/09/160.483A
FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2025
TYPE: DNA
ORGANISM: mus.musculus domesticus
US-09-160-483-2

Query Match
82.0%: Score 16.4; DB 3; Length 2025;
Best Local Similarity 94.4%: Pred. No. 1.1e+02;
Matches 17: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 cgcgcgcgcgcgcgcgc 18
 DB 87 CCGCCGCCGCCGCCGCC 70

RESULT 9
 US-08-890-853-3/C

Sequence 3. Application US/08890853

Patent No. 5851812

GENERAL INFORMATION:

APPLICANT: Goeddel, David V.

INVENTOR: Goeddel, David V.

TITLE OF INVENTION: IKK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: US

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/890.853

APPLICATION NUMBER: US/08/890.853

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 797-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2238 base pairs

STRANDEDNESS: double

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-890-853-3

Query Match 82.0%; Score 16.4; DB 2; Length 2238;
 Local Similarity 94.4%; Pred.No.1e+02; 1; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgcgcgcgcgcgcgcgc 18
 DB 34 CCGCCGCCGCCGCCGCC 17

RESULT 10
 US-09-099-125A-3/C

Sequence 3. Application US/0909125A

Patent No. 5916760

GENERAL INFORMATION:

APPLICANT: Goeddel, David V.

INVENTOR: Morimoto, John

TITLE OF INVENTION: IKK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: US

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/099.124A

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 797-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099.125A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/890.853

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 797-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2238 base pairs

STRANDEDNESS: double

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-099-125A-3

Query Match 82.0%; Score 16.4; DB 2; Length 2238;
 Best Local Similarity 94.4%; Pred.No.1e+02; 1; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgcgcgcgcgcgcgcgc 18
 DB 34 CCGCCGCCGCCGCCGCC 17

RESULT 11

US-09-099-124A-3/C

Sequence 3. Application US/0909124A

Patent No. 593302

GENERAL INFORMATION:

APPLICANT: Goeddel, David V.

INVENTOR: Morimoto, John

TITLE OF INVENTION: IKK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: US

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/099.124A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/890.853

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 797-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 2238 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-032-476-3

Query Match 82.0%: Score 16.4; DB 2; Length 2238;
Best Local Similarity 94.4%: Pred. No. 1e+02;
Matches 17: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgcgcctcgccgcgcgc 18
 34 cccgcgccgcgcgcgcgc 17
DB

RESULT 12
US-09-032-476-3/C
Sequence 3, Application US/09032476
PATENT NO. 6235512
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: TECHNOLOGY LAM GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,476
FILING DATE:
CLASSIFICATION:
PUBLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 797-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2238 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-032-476-3

Query Match 82.0%: Score 16.4; DB 4; Length 2238;
Best Local Similarity 94.4%: Pred. No. 1e+02;
Matches 17: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgcgcctcgccgcgcgc 18
 34 cccgcgccgcgcgcgcgc 17
DB

RESULT 13
US-08-890-854-3/C
Sequence 3, Application US/08890854
PATENT NO. 6235512
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 797-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2238 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-890-854-3

Query Match 82.0%: Score 16.4; DB 4; Length 2238;
Best Local Similarity 94.4%: Pred. No. 1e+02;
Matches 17: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgcgcctcgccgcgcgc 18
 34 cccgcgccgcgcgcgcgc 17
DB

RESULT 14
US-09-023-324-3/C
Sequence 3, Application US/09023324
PATENT NO. 6235513
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
FILING DATE: ON:
PRIORITY DATE: ON:
PRIOR APPLICATION NUMBER: 08/890,854
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
INVENTOR INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2238 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-023-324-3

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```

Query Match          82.0%  Score 16.4;  DB 4;  Length 2238;
Database: nt          34.4%  Pred. No. 1e+02;  1;  Indels  0;  Gaps  0;
Matches 17;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

QY      1  cgcgcgcgcgcgcgcgc 18
        ||||| ||||| |||||
DB      34  CCGCGCCGCCGCCGACCC 17

```

```

RESULT 15
US-08-910-820-7/c
Sequence 7, Application US/08910820
Patent No. 6258579
GENERAL INFORMATION:
APPLICANT: MERCURIO, Frank
INVENTOR: MURRAY, Brian W.
APPLICANT: Barbois Miguel
APPLICANT: LI, Gian
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
SEQUENCE SEQUENCE:
ADDRESS: SEED BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
SOFTWARE: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
PRIORITY DATE: 08-08-1997
ATTORNEY/AGENT INFORMATION:
NAME: MCKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098,413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
FAX: (206) 682-0031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2251 base pairs

```

```

TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
US-08-910-820-7

```

```

Query Match          82.0%  Score 16.4;  DB 4;  Length 2251;
Database: nt          34.4%  Pred. No. 1e+02;  1;  Indels  0;  Gaps  0;
Matches 17;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

QY      1  cgcgcgcgcgcgcgcgc 18
        ||||| ||||| |||||
DB      47  CCGCGCCGCCGCCGACCC 30

```

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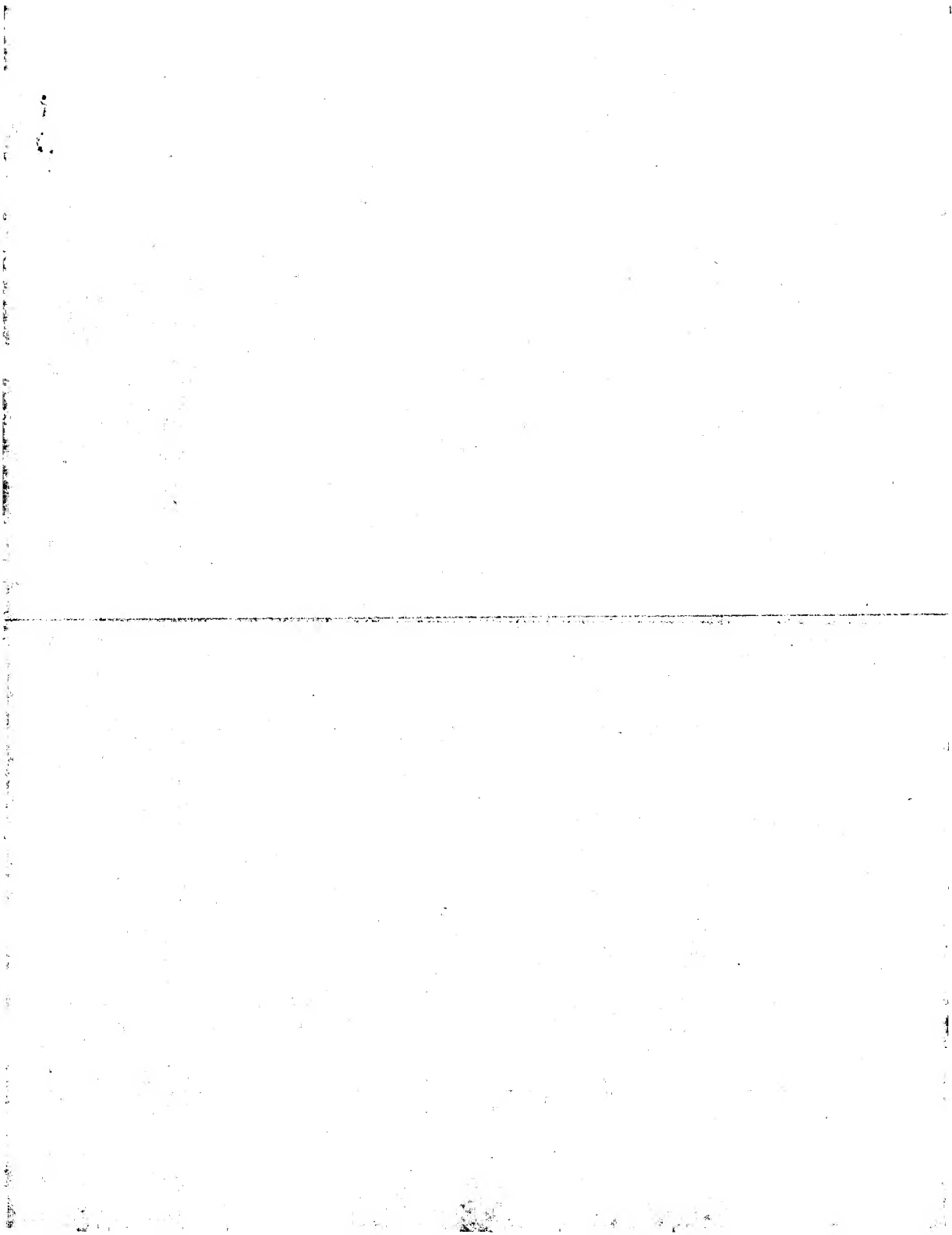
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Tue Jun '25 08:50:00 2002

us-09-747-514a-1.rni

Page 7



JOURNAL Submitted (11-OCT-1995) Paul W. Hager, Microbiology & Immunology,
East Carolina University, Greenville, NC 27856, USA
COMMENT On Nov 29, 1995 this sequence version replaced g1:496210.
FEATURES Location/Qualifiers
SOURCE

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1-diphosphate; Method: conceptual translation supplied by
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BASE COUNT 551 a 1020 c 985 g 563 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cv 1 gttacagcgtttatcactacagcg 24
|||||
Db 1418 gttacagcgtttatcactacagcg 1395

comp

RESULT 2
AE004946 13075 bp DNA linear BCT 30-NOV-2000
LOCUS
Pseudomonas aeruginosa PA01, section 507 of 549 of the complete
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

genome: AE004091
AE004946.1 GI:951650
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.

REFERENCE
AUTHORS

1 (bases 1 to 13075)
Stover C.C., Pham X.Q., Erwin A.L., Mizoguchi S.D., Warrenner P.,
Hickey M.J., Brinkman F.S.L., Huftnagle W.C., Kowalik D.J.,
Brodie L.L., Coulter S.N., Folger K.R., Kass A., Larbig K., Lim R.,
Smith K., Spencer D., Wong G.K., Wu Z. and Paulsen I.T.
Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
2 (bases 1 to 13075)
Stover C.C., Pham X.Q., Erwin A.L., Mizoguchi S.D., Warrenner P.,
Hickey M.J., Brinkman F.S.L., Huftnagle W.C., Kowalik D.J.,
Lagrou M., Garber R.L., Gulyuz L., Tolentino E.,
Westbrook-Webster S., Yuan Y., Brody L.L., Coulter S.N.,
Folger K.R., Kass A., Larbig K., Lim R.M., Smith K.A., Spencer D.H.,
Wong G.K.S., Wu Z., Paulsen I.T., Reiter J., Sater M.H.,
Bancroft R.E., Lacey S. and Olson R.V.
Submitted (16-MAY-2000) Department of Medicine and Genetics,
University of Washington Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA

TITLE

JOURNAL
FEATURES
source

gene

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FEATURES

98195-7242, USA

Location/Qualifiers

Source

1. .11208

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Washington) •

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Best Local Similarity 86.4%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      3  largecctgaagctgacgca 24
Db      1737  TCCCGCTCGAAGCATGCGCCG 1706

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DEFINITION Agrobacterium tumefaciens str. C58 linear chromosome, section 148
of 187 of the complete sequence.
ACCESSION  ARO08344 AB007870
VERSION    ARO08344.1 GI:15159976
KEYWORDS
SOURCE     Agrobacterium tumefaciens str. C58 (Cereon).
ORGANISM   Agrobacterium tumefaciens str. C58 (Cereon)
            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
            Rhizobiaceae; Rhizobium.
REFERENCE  1 (bases 1 to 12819)
AUTHORS   Hinkle,G., Slater,S.C. and Goodner,B.
TITLE     Complete Genome Sequence of Agrobacterium tumefaciens C58
            (Rhizobium radiobacter C58), the Causative Agent of Crown Gall
            Disease in Plants
            2 (bases 1 to 12819)
            Direct Submission
            Hinkle,G., Slater,S.C. and Goodner,B.
JOURNAL   Submitted (14-AUG-2001) Bioinformatics, Cereon Genomics, 45 Sidney
            Street, Cambridge, MA 02139, USA
            Approximately 800 bp of telomeric sequence missing from the left
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COMMENT   Local 12819
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CDS

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2002, 14:59:54 : Search time 652.13 Seconds
(without alignments)
63.187 Million cell updates/sec

Title: US-09-747-514a-2

Perfect score: 24

Sequence: 1 gtagagcccgtaacgacgacg 24

Scoring table: IDENTITY, NUC
Gapop 10.0 , Gapext 1.0

Searched: 173636 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008
Limiting filter 45 summaries

Database :

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	17.6	73.3	927	22	AAH6133	C glutamicum codin
C 2	17.6	73.3	30940	22	AAH6133	C glutamicum codin
C 3	16.6	67.5	23128	22	AAH7078	Propionibacterium
C 4	16.2	69.2	983	22	AAH7078	Proliferative gl
C 5	16.2	67.5	1386	22	AAH7078	Mouse nuclear pro
C 6	16.2	67.5	4383	23	AB107815	Human immune sy
C 7	16.2	67.5	5660	24	AB134357	Human immune sy
C 8	16.2	67.5	7690	23	AB107814	Dicapsophylla melo
C 9	16	66.7	671	21	AAH13425	Aspergillus oryzae

C 10	15.8	65.8	549	16	AAH80147	DNA fragment func
C 11	15.8	65.8	549	16	AAH92906	Corynebacterium 549 bp
C 12	15.8	65.8	549	19	AAH15033	Promoter from B.fl
C 13	15.8	65.8	551	16	AAH80346	DNA fragment func
C 14	15.8	65.8	551	16	AAH72932	Corynebacterium 551 bp
C 15	15.8	65.8	551	16	AAH72932	Promoter from B.fl
C 16	15.8	65.8	825	22	AAH89278	Escherichia coli P
C 17	15.8	65.8	6921	22	AAH89273	Escherichia coli P
C 18	15.8	65.8	750	20	AAH87760	EST clone BQ215
C 19	15.6	65.0	1338	21	AAH12622	Aspergillus oryzae
C 20	15.6	65.0	2475	23	AAH53040	DNA encoding novel
C 21	15.6	65.0	3042	23	AAH53042	DNA encoding novel
C 22	15.6	65.0	3266	23	AAH52872	DNA encoding novel
C 23	15.6	65.0	6235	24	AB132787	Human immune syste
C 24	15.6	65.0	6650	24	AB103869	Drosophila melanog
C 25	15.6	65.0	31562	23	AB103868	Drosophila melanog
C 26	15.6	65.0	4403765	22	AA199688	Mycobacterium tube
C 27	15.6	65.0	4403765	22	AA199688	Mycobacterium tube
C 28	15.6	65.0	4403765	22	AA199688	Mycobacterium tube
C 29	15.6	65.0	4403765	22	AA199688	Mycobacterium tube
C 30	15.6	65.0	4403765	22	AA199688	Mycobacterium tube
C 31	15.4	64.2	21429	22	AAH57463	DNA encoding recomb
C 32	15.2	63.3	845	17	AAH11323	DNA encoding recomb
C 33	15.2	63.3	873	22	AAH67645	P. putida oxydinas
C 34	15.2	63.3	897	22	AAH67645	P. putida oxydinas
C 35	15.2	63.3	931	22	AAH71051	Proteobacterium glom
C 36	15.2	63.3	984	22	AAH71599	Corynebacterium gl
C 37	15.2	63.3	1164	21	AAH43106	Arabisidopsis thalia
C 38	15.2	63.3	1164	21	AAH43106	Arabisidopsis thalia
C 39	15.2	63.3	1229	23	AAH64885	DNA encoding novel
C 40	15.2	63.3	1314	21	AAH64885	Bordetella pertuss
C 41	15.2	63.3	1630	15	AAH66684	Acv B2 gene - enco
C 42	15.2	63.3	1632	22	AAH61090	P. putida K12440-a
C 43	15.2	63.3	2033	21	AAH60796	Arabisidopsis thalia
C 44	15.2	63.3	2559	23	AAH50525	Drosophila melanog
C 45	15.2	63.3	2729	10	AAH92629	DNA fragment conta

ALIGNMENTS

RESULT 1	AAH6133/	DNA: 927 BP.
AAH6133 standard:	DNA: 927 BP.	
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AC	AAH6133:	
DT	26-SEP-2001 (first entry)	
DE	C glutamicum coding sequence fragment SEQ ID NO: 3168.	
DE	C glutamicum coding sequence fragment SEQ ID NO: 3168.	
XX	Corynebacterium; amino acid synthesis; vitamin; saccharide;	
KW	organic acid synthesis; de.	
XX		
OS	Corynebacterium glutamicum.	
XX		
FN	EP108790-A2.	
XX		
XX	20-JUN-2001.	
XX		
XX	18-DEC-2000; 2000EP-0127688.	
XX		
PR	16-DEC-1999; 93JP-0377484.	
PR	07-APR-2000; 2000JP-0159162.	
PR	03-AUG-2000; 2000JP-0280988.	
XX		
XX	(KYO) KYOKA HAKKO KOGYO KK.	
PI	Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;	
XX	Tateishi N, Senoh A, Ikeda M, Ozaki A.	
XX	WPI: 2001-376931/40.	
DR	P-PSDB: AAH92914.	

Db 956 GGCAGGGCCCTANAGATCGGC 935

Db 956 GGCAGGGCCCGTANAGATCGGC 935

PT	uses fluorescence-labeled nucleic acids isolated from the cells and a
PF	substrate of expressed sequence tags -
XX	
PY	
XX	Claim 88: Page 2456; 3161pp; Enghlsh.
CC	
CC	The present invention describes a method for monitoring differential
CC	expression of genes in a first filamentous fungus relative to
CC	expression of the same genes in one or more second filamentous
CC	cells. The method uses fluorescence-labeled nucleic acids isolated from
CC	the PF cells and a substrate of expressed sequence tags (EST). The ESTs
CC	are used in the methods for monitoring differential expression of genes
CC	in a first filamentous fungal (PF) cell relative to expression of the
CC	genes in one or more second filamentous fungal cells. Monitoring the
CC	differential expression of genes allows the production
CC	potential of the microorganisms to be studied. The method can be
CC	disclosed, possible functions of unknown open reading frames can be
CC	identified and gene copy number variation and stability can be
CC	monitored. The expression of genes can be used to study how PF cells
CC	adapt to changes in culture conditions, environmental stress, spore
CC	morphogenesis, recombination, metabolic or catabolic pathway
CC	random DNA cloning. ESTs provides several advantages over genomic or
CC	array equals one gene or open reading frame. Redundancy as one spot on an
CC	microarrays based on function of the gene products to facilitate
CC	analysis of the results. AA074478 to AAF1247 represents ESTs from
CC	Fusarium venenatum. AAF1248 to AAF1853 represents ESTs from Aspergillus
CC	niger; AAF1854 to AAF1937 represents ESTs from Aspergillus oryzae; and
CC	AA15679 to AA15737 represents ESTs from Trichoderma reesei, which are
CC	all specifically claimed in the present invention.
XX	
SQ	Sequence 671 BP; 183 A; 179 C; 175 G; 132 T; 2 other;
DB	
OY	1 gtagagccgcacgacgacggcg 24
DB	
DB	522 gctagcgaactaaatgccgcg 545
RESULT 10	
AD	AAG080477 standard; DNA, 549 BP.
LD	AAG080347 standard; DNA, 549 BP.
AC	AA080347;
DT	11-SEP-1995 (first entry)
DE	DNA fragment functional as a promoter in Corynebacterium.
KM	Promoter: Corynebacterium bacterium; Brevibacterium flavum; enzyme;
KW	gene expression); biosynthesis; amino acid; organic acid; lipid; protein; fat; oil; antidiabetic; GS.
OS	Brevibacterium flavum MJ-233 (FERM BP-1497).
XX	
XX	EP629699-A.
XX	
PD	21-DEC-1994.
PP	
PF	07-JUN-1994; 94BP-0108738.
XX	
PR	15-JUN-1993; 93US-0076091.
XX	
PI	(ATIP) MITSUBISHI PETROCHEMICAL CO LTD.
XX	
XX	Yukawa H., Zupancic TJ.
DR	WPI; 1995-024246/04.
XX	
XT	DNA fragment from corynebacter bacteria with promoter activity -

PT expresses the gene of interest in coryneform bacteria at a high
rate and has a greater promoter strength than a tac promoter

Claim 13: Page 58: 67pp: English.

XX The promoter DNA fragment can be used to express a gene of interest
CC in coryneform bacteria at a greater strength than a tac promoter used for
CC expression of a gene of interest in coryneform bacteria.
CC Coryneform bacteria. The promoter fragment may be used to express
CC genes products such as enzymes involved in biosynthesis and
CC metabolism of bio-substances e.g. amino acids, organic acids,
CC vitamins, lipids, and enzymes involved in the biosynthesis and
CC metabolism of bioactive substances such as proteins, fatty acids
CC and antibiotics. Twenty sequences are provided, each with a unique
CC site (see SEQ ID NO: 133-152). This promoter is controllable
CC by replacing ethanol in the culture medium with glucose.

XX Sequence 549 BP: 122 A; 131 C; 143 G; 153 T; 0 other;

Query Match 65.8%; Score 15.8; DB 16; Length 549;

Best Local Similarity 89.5%; Pred. No. 2.6e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4 agcgccgtaacgacgcg 22

177 AGCGCGTGAACGACGCGC 159

DB

RESULT 11

AAAT92906/C

ID AAAT92906 standard; DNA: 549 BP.

AC AAAT92906;

DT 27-APR-1998 (first entry)

DK Coryneform 549 bp promoter fragment.

XX Promoter: coryneform bacterium; gene expression: ds.

XX Brevibacterium flavum MJ-233 (FERM BP-1497).

XX EP803575-A1.

XX 29-OCT-1997.

PF 07-JUN-1994: 94AP-0108382.

PR 15-JUN-1993: 93US-0076091.

XX (MITU) MITSUBISHI CHEM CORP.

XX Yukuwa H., Zupancic TJ;

PI WPI: 1997-515322/48.

DR Promoter for gene expression in coryneform bacteria - used for

XX controllable expression of genes by changing carbon source in

PT culture medium

XX Claim 2: Page 48: 58pp: English.

XX This novel isolated DNA fragment is functional as a promoter in
CC coryneform bacteria. It has greater strength of the DNA fragment is
CC than the prior art promoter. The promoter fragment may be used to express
CC a gene of interest in coryneform bacteria.
CC The promoter fragment may be used to express a gene of interest in
CC coryneform bacteria containing the DNA fragment. Claimed
CC promoter fragments (AAAT92904-11) can be used for externally
CC controllable expression of genes in coryneform bacteria, e.g.
CC microbial, animal or plant genes encoding enzymes involved in the
CC biosynthesis or metabolism of substances such as amino acids,
CC organic acids, vitamins, lipids, proteins, fats, oils or

CC antibiotics. All are derived from Brevibacterium flavum MJ233
CC chromosomal DNA. They were obtained by inserting Alu-HaeIII
CC restriction fragments of the DNA into the promoter probe shuttle
CC vector pPROBE17 at its PstI site.

XX Sequence 549 BP: 122 A; 131 C; 143 G; 153 T; 0 other;

Query Match 65.8%; Score 15.8; DB 16; Length 549;

Best Local Similarity 89.5%; Pred. No. 2.6e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4 agcgccgtaacgacgcg 22

177 AGCGCGTGAACGACGCGC 159

DB

RESULT 12

AAAT15032

ID AAAT15033 standard; DNA: 549 BP.

AC AAAT15033;

DT 28-MAY-1998 (first entry)

DK Promoter from B. flavum MJ233 K6101.

XX Promoter: coryneform bacteria; genetic engineering;

XX gene expression control; ds.

XX Brevibacterium flavum.

XX US5726299-A.

XX 10-MAR-1998.

PF 01-AUG-1994: 94US-0285641.

PR 01-AUG-1994: 94US-0285641.

PR 03-JUN-1994: 93US-0076091.

XX 15-JUN-1993: 93US-0076091.

XX (MITU) MITSUBISHI CHEM CORP.

XX Yukuwa H., Zupancic TJ;

PI WPI: 1998-192831/17.

DR Coryneform bacteria promoter sequence(s) - controllable by change in

XX culture medium

XX Claim 10: column 55-66: 40pp: English.

XX This sequence represents a promoter from Brevibacterium flavum, and is an

CC example of the sequence of the invention. The sequence is a DNA

CC fragment obtained from a coryneform bacteria, and which functions as a

CC promoter. The promoter's function is controlled by: (a) removing at least

CC one substance from a coryneform bacteria culture medium; (b) adding at

CC least one substance which is assimilable by coryneform bacteria; or for

CC (c) both (a) and (b). The promoter is useful in genetic engineering, or for

CC controlling expression of genes of interest in coryneform bacteria.

RESULT 13
 XN ANV15032/C
 XX TMO80346 standard; DNA: 551 BP.
 XX
 AC AAO80346;
 XX
 DT 11-SEP-1995 (first entry)
 XX
 DE DNA fragment functional as a promoter in *Corynebacterium* bacteria.
 XX
 KW Promoter: *Corynebacterium* bacterium; *Brevibacterium* flavum; enzyme;
 KW gene expression; biosynthesis; photo-synthesis; amino substance; vitamin;
 KW amino acid; organic acid; lipid; protein; etc; oil; antibiotic; ds.
 XX
 OS *Brevibacterium* flavum MJ-233 (FERM BP-1497).
 XX
 XN EP626699-A.
 XX
 PD 21-DEC-1994.
 XX
 PF 07-JUN-1994: 94EP-0108738.
 XX
 PR 15-JUN-1993: 93US-0076091.
 XX
 PA (MTP) MITSUBISHI PETROCHEMICAL CO LTD.
 XX
 PI Yukawa H, Zupancic TJ;
 XX
 DR WPI: 1995-024246/04.
 XX
 XX DNA fragment from *Corynebacterium* bacteria with promoter activity -
 XX assesses the gene of interest in *Corynebacterium* bacteria at a high
 XX rate and has a greater promoter strength than a tac promoter
 XX
 PS Claim 12: Page 58; 67pp: English.
 XX
 CC The promoter DNA fragment can be used to express a gene of interest
 CC in *Corynebacterium* bacteria at a high level. It may also be used for
 CC the expression of a gene of interest in *Corynebacterium* bacteria.
 CC *Corynebacterium* bacteria.
 CC gene products such as enzymes involved in the biosynthesis and
 CC metabolism of bio-substances e.g. amino acids, organic acids,
 CC vitamins, lipids; and enzymes involved in the biosynthesis and
 CC metabolism of bioactive substances such as proteins, fats and oils
 CC and antibiotics. Twenty sequences with such promoter activity
 CC are selected (see also AAO80333-52). This promoter is controllable
 CC by replacing glucose in the culture medium with ethanol.
 XX
 SO Sequence 551 BP; 126 A; 130 C; 138 G; 157 T; 0 other;

Query Match 65.88; Score 15.8; DB 16; Length 551;
 Best Local Similarity 89.58; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 4 aagccgcgcgaacatcgcgc 22
 ||||| | ||||| |||||
 Db 176 AGCCGCTGGAACGATCCGC 158

RESULT 14
 ANV92905/C
 ID AAT92905 standard; DNA: 551 BP.
 AC AAT92905;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE *Corynebacterium* 551 bp promoter fragment.
 XX
 KW Promoter: *Corynebacterium* bacterium; gene expression; ds.
 XX

OS *Brevibacterium* flavum MJ-233 (FERM BP-1497).
 XX
 XN EP803575-A1.
 XX
 PD 29-OCT-1997.
 XX
 PF 07-JUN-1994: 94EP-0108382.
 XX
 PR 15-JUN-1993: 93US-0076091.
 XX
 PA (MTP) MITSUBISHI CHEM CORP.
 XX
 PI Yukawa H, Zupancic TJ;
 XX
 DR WPI: 1997-515322/48.
 XX
 XX Promoters for gene expression in *Corynebacterium* bacteria - used for
 XX controllable expression of genes by changing carbon source in
 XX culture medium
 XX
 PS Claim 1: Page 48; 58pp: English.
 XX
 CC This novel isolated DNA fragment is functional as a promoter in
 CC *Corynebacterium* bacteria. It has greater strength in *Corynebacterium* cells
 CC than the tac promoter. The promoter DNA fragment is functional as
 CC for a *Corynebacterium* bacterium containing the DNA fragment. Claimed
 CC promoter fragments (AAT92904-11) can be used for externally
 CC controllable expression of genes in *Corynebacterium* bacteria, e.g.
 CC microbial, animal or plant genes encoding enzymes involved in the
 CC metabolism of substances such as amino acids,
 CC organic acids, vitamins, lipids; and enzymes involved in the
 CC biosynthesis and metabolism of bio-substances such as proteins, fats and
 CC antibiotics. All are derived from *Brevibacterium* MJ233
 CC chromosomal DNA. They were obtained by inserting Alu-HaeII
 CC restriction fragments of the DNA into the promoter probe shuttle
 CC vector PROBE8T at its EcoRV site.
 XX
 SO Sequence 551 BP; 126 A; 130 C; 138 G; 157 T; 0 other;

Query Match 65.88; Score 15.8; DB 18; Length 551;
 Best Local Similarity 89.58; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 4 aagccgcgcgaacatcgcgc 22
 ||||| | ||||| |||||
 Db 176 AGCCGCTGGAACGATCCGC 158

RESULT 15
 ANV15032/C
 ID AAT15032 standard; DNA: 551 BP.
 AC AAT15032;
 XX
 DT 28-MAY-1998 (first entry)
 XX
 DE Promoter from *B. flavum* MJ233 RE102.
 XX
 KW Promoter: *Corynebacterium* bacteria; genetic engineering;
 KW gene expression control; ds.
 XX
 OS *Brevibacterium* flavum.
 XX
 XN US5726299-A.
 XX
 PD 10-MAR-1998.
 XX
 PF 01-AUG-1994: 94US-0285641.
 XX
 PR 01-AUG-1994: 94US-0285641.
 XX
 PR 01-JUN-1993: 93US-0709151.
 XX
 PR 15-JUN-1993: 93US-0076091.

XX (MITU) MITSUBISHI CHEM CORP.
XX
XX

PI Yukawa H, Zupancic TJ;
XX

DR WPI: 1998-192831/17.
XX

XX Coryneform bacteria promoter sequence(s) - controllable by change in
XX culture medium
XX

PS Claim 9: column 63-64: 40pp; English.
XX

XX This sequence represents a promoter from *Brevibacterium flavum*, and is an
XX example of the DNA sequence used to control gene expression in a
XX Coryneform bacteria, and which functions as a
XX promoter. The promoter's function is controlled by: (a) removing at least
XX one substance from a coryneform bacteria culture medium; (b) adding at
XX least one substance which is assimilable by coryneform bacteria; or
XX (c) both (a) and (b). The promoter is useful in genetic engineering for
XX controlling expression of genes of interest in coryneform bacteria.
XX

SQ Sequence 551 BP: 126 A; 130 C; 138 G; 157 T; 0 other:
XX

Query Match 65.8%; Score 15.8; DB 19; Length 551;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX

OY 4 agcgccgctacacgacgcgc 22
XXXXXXXXXXXXXXXXXXXX

DB 176 ACCGCTCGAACGATCGCG 158
XXXXXXXXXXXXXXXXXXXX

Search completed: June 23, 2002, 15:00:17
Job time: 8119 sec

IDENTIFICATION METHOD: experiment
US-08-076-091C-15

Query Match 65.8% Score 15.8; DB 1: Length 549;
Best Local Similarity 89.5% Pred. No. 46;
Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 agagcccgtaacgatgcgc 22
||||| |||||||
DB 177 AGGCGCTGAGACGATGCGC 159

RESULT 2

US-08-285-641-15/C
Sequence 15, Application US/08285641
Patent No. 5726299
GENERAL INFORMATION:
APPLICANT: Zupancic, Thomas J.
APPLICANT: Yukawa, Hideaki
TITLE OF INVENTION: PROMOTER DNA FRAGMENT FROM CORNNEFORM BACTERIA
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zimm, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER:
OPERATING SYSTEM:
SOFTWARE:
CURRENT APPLICATION DATA:
PILING DATE: 11-AUGUST-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076,091
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: US 07/709,151
PILING DATE: 19-MAY-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 base pairs
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORGANISM: Brevibacterium Flavum
STRAIN: MJ-233
FEATURE:
NAME/KEY: promoter
LOCATION: 1-549
IDENTIFICATION METHOD: experiment
US-08-285-641-15

Query Match 65.8% Score 15.8; DB 1: Length 549;
Best Local Similarity 89.5% Pred. No. 46;
Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 agagcccgtaacgatgcgc 22
||||| |||||||
DB 177 AGGCGCTGAGACGATGCGC 159

RESULT 3

US-08-076-091C-14/C

Sequence 14, Application US/08076091C
Patent No. 5726299
GENERAL INFORMATION:
APPLICANT: Zupancic, Thomas J.
APPLICANT: Yukawa, Hideaki
TITLE OF INVENTION: PROMOTER DNA FRAGMENT FROM CORNNEFORM BACTERIA
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: Mion, Zimm, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: CORNNEFORM
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,091C
FILING DATE: 15-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/709,151
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-32650
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 12037060
TELEFAX: (202) 293-7860
TELEX: 6491103

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 551 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium Flavum
STRAIN: MJ233
FEATURE:
NAME/KEY: promoter
LOCATION: 1-551
IDENTIFICATION METHOD: experiment
US-08-076-091C-14

Query Match 65.8% Score 15.8; DB 1: Length 551;
Best Local Similarity 89.5% Pred. No. 46;
Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 agagcccgtaacgatgcgc 22
||||| |||||||
DB 176 AGGCGCTGAGACGATGCGC 158

RESULT 4

US-08-285-641-14/C

Sequence 14, Application US/08285641
Patent No. 5726299
GENERAL INFORMATION:
APPLICANT: Zupancic, Thomas J.
APPLICANT: Yukawa, Hideaki
TITLE OF INVENTION: PROMOTER DNA FRAGMENT FROM CORNNEFORM BACTERIA
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

```

ADDRESSER: Sughrue, Mion, Zim, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER:
OPERATING SYSTEM:
SEQUENCE:
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/285,641
  FILING DATE: 1-AUGUST-1994
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/076,091
    FILING DATE: 13-JUN-1993
    FILING DATE: 29-MAY-1991
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:
    TELEFAX:
  TELETYPE:
  INFORMATION FOR SEQ ID NO: 14:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 551
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
    MOLECULE TYPE: genomic DNA
    ORGANISM: Brevibacterium flavum
    FEATURE:
      NAME/KEY: promoter
      LOCATION: 1-551
      IDENTIFICATION METHOD: experiment
US-08-285-641-14

Query Match
Best Local Similarity: 65.8% Score 15.8; DB 1; Length 551;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 agcgccctaacgacgcgc 22
Db 176 AGCGCCCTGAACGATCGC 158

RESULT 5
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
  APPLICANT: FLEISCHMAN, Robert D.
  APPLICANT: WHITE, Owen R.
  APPLICANT: FRASER, Claire M.
  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
  FILE REFERENCE: 24366-20007.00
  CURRENT APPLICATION NUMBER: US/09/103,840A
  NUMBER OF SEQ ID NOS: 2
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 2
  LENGTH: 4403765
  TYPE: DNA
  ORGANISM: Mycobacterium tuberculosis
  OTHER INFORMATION: CDC 1551
  OTHER INFORMATION: "n" bases at various positions throughout the sequence

```

```

OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match
Best Local Similarity: 65.0% Score 15.6; DB 4; Length 4403765;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 1 gctagccgcctaacgacgcgcg 24
Db 4027823 gctcgtccgctaacgacgcgcg 4027846

RESULT 6
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
  APPLICANT: FLEISCHMAN, Robert D.
  APPLICANT: WHITE, Owen R.
  APPLICANT: FRASER, Claire M.
  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
  FILE REFERENCE: 24366-20007.00
  CURRENT APPLICATION NUMBER: US/09/103,840A
  CURRENT FILING DATE: 1998-06-24
  CURRENT OF SEQ ID NOS: 2
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 2
  LENGTH: 4403765
  TYPE: DNA
  ORGANISM: Mycobacterium tuberculosis
  FEATURE:
    NAME/KEY: CDC 1551
    LOCATION: 1-4403765
    IDENTIFICATION METHOD: represent a, t, c or g
US-09-103-840A-2

Query Match
Best Local Similarity: 85.7% Score 15.6; DB 4; Length 4403765;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 3 ttcgcccgcctaacgacgcgcg 23
Db 1537086 TAGCAGCCGTGACGATCGACG 1537066

RESULT 7
US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
  APPLICANT: FLEISCHMAN, Robert D.
  APPLICANT: WHITE, Owen R.
  APPLICANT: FRASER, Claire M.
  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
  FILE REFERENCE: 24366-20007.00
  CURRENT APPLICATION NUMBER: US/09/103,840A
  CURRENT FILING DATE: 1998-06-24
  NUMBER OF SEQ ID NOS: 2
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 1
  LENGTH: 4411529
  TYPE: DNA
  ORGANISM: Mycobacterium tuberculosis
  OTHER INFORMATION: H37Rv
US-09-103-840A-1

```


CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/266,451
 FILING DATE: 23-JUNE-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Loch, Karen F.
 REGISTRATION NUMBER: 35,238
 REFERENCE/DOCKET NUMBER: 00786/219002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 845
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-748-725-1

Query Match 63.38; Score 15.2; DB 2; Length 845;
 Best Local Similarity 85.08; Pred. No. 89;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 gtagccgcgaacatgcag 21

Db 147 gtagccgcgaacatgcag 128

RESULT 11

5240849-4
 Patent No. 5240849
 APPLICANT: Akiyama, Akira; Kawamura, Naoto; Kojima, Ikou; Okumura, Yasuaki; Okumura, Hiroshi; Toge, Okumura, Hiroshi
 TITLE OF INVENTION: METHOD FOR IDENTIFYING A DNA SEQUENCE CAPABLE OF ACTIVATING THE "A" POSITION OF MACROIDE ANTIBIOTIC
 NUMBER OF SEQUENCES: 5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/06/353,323
 FILING DATE: 23-MAY-1989
 SEQ ID NO: 4:
 LENGTH: 1164
 5240849-4

Query Match 63.38; Score 15.2; DB 6; Length 1164;
 Best Local Similarity 85.08; Pred. No. 89;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 gtagccgcgaacatgcag 24

Db 506 gtagccgcgaacatgcag 525

RESULT 12

5240849-1
 Patent No. 5240849
 APPLICANT: Akiyama, Akira; Kawamura, Naoto; Kojima, Ikou; Okumura, Yasuaki; Okumura, Hiroshi; Toge, Okumura, Hiroshi
 TITLE OF INVENTION: DNA CODING FOR ENZYME CAPABLE OF ACTIVATING THE "A" POSITION OF MACROIDE ANTIBIOTIC
 NUMBER OF SEQUENCES: 5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/06/353,323
 FILING DATE: 23-MAY-1989
 SEQ ID NO: 1:
 LENGTH: 2749
 5240849-1

Query Match 63.38; Score 15.2; DB 6; Length 2749;
 Best Local Similarity 85.08; Pred. No. 90;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 gtagccgcgaacatgcag 24

Db 2074 gtagccgcgaacatgcag 2093

RESULT 13

US-08-390-878-16
 Sequence 16, Application US/08390878
 Patent No. 5700683
 GENERAL INFORMATION:
 APPLICANT: Slover, Charles K.
 ATTORNEY/AGENT INFORMATION:
 NAME: Slover, Charles K.
 REGISTRATION NUMBER: 18
 TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: One Market Plaza, Stuart Street Tower, 20th
 STREET: Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION RELEASE #1.0, Version #1.30

APPLICATION NUMBER: US/08/390,878

FILING DATE: 17-FEB-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

TELEPHONE: 415/543/9600

TELEFAX: 415/543/5043

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 1685 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear, single

MOLECULE TYPE: DNA (genomic)

US-08-390-878-16

Query Match 63.38; Score 15.2; DB 1; Length 1685;
 Best Local Similarity 85.08; Pred. No. 93;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 gtagccgcgaacatgcag 24

Db 16069 gtagccgcgaacatgcag 16088

RESULT 14

US-08-325-477B-2/C
 Sequence 2, Application US/08225477B
 Patent No. 5635370
 GENERAL INFORMATION:
 APPLICANT: Susan Hockfield
 ATTORNEY/AGENT INFORMATION:
 NAME: Slover, Charles K.
 REGISTRATION NUMBER: 18
 TITLE OF INVENTION: BRAIN HYPER-INDUCING PROTEIN
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: St. Onge Steward Johnston & Reens
 STREET: 966 Bedford Street
 CITY: Stamford

STATE: CT
 COUNTRY: United States
 ZIP: 06905
 COMPUTER READABLE FORM:
 COMPUTER TYPE: IBM PC
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Word Processor
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/225.4778
 FILING DATE: April 8, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Mary M. Kinisky
 REGISTRATION NUMBER: 32423
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 203-324-6155
 TELEFAX: 203-327-1096
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1519 bases
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA encoding a protein
 DESCRIPTION: entire sequence
 FRAGMENT TYPE: entire sequence
 FEATURE:
 NAME/KEY: cat brain BEHAB
 US-08-225-4778-2

Query Match 62.5% Score 15; DB 1; Length 1519;
 Best Local Similarity 78.3%; Pred. No. 1.1e+02;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 ggtacgcccgtacgctccgccc 23
 DB 1209 ggtacgcccgtccctccgccc 1187

RESULT 15
 PCT-0595-04353-2/G
 Sequence 2, Application PC/TUS9504353
 GENERAL INFORMATION:
 APPLICANT: Susan Hockfield
 TITLE OF INVENTION: BEHAB, A Brain Hyaluronan Binding Protein
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: St. Onge Steward Johnston & Reems
 STREET: 986 Bedford Street
 CITY: Stamford
 STATE: CT
 COUNTRY: United States
 PCT-0595-04353-2/G
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" 1.44 Mb diskette
 COMPUTER: IBM PC
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Word Processor
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/0595/04353
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/225.477
 FILING DATE: April 8, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Mary M. Kinisky
 REGISTRATION NUMBER: 32423
 REFERENCE/DOCKET NUMBER: 1751-P0004

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 203-324-6155
 TELEFAX: 203-327-1096
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1519 bases
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA encoding a protein
 DESCRIPTION: entire sequence
 FRAGMENT TYPE: entire sequence
 IMMEDIATE SOURCE: cat cortex
 FEATURE:
 NAME/KEY: cat brain BEHAB
 PCT-0595-04353-2

Query Match 62.5% Score 15; DB 5; Length 1519;
 Best Local Similarity 78.3%; Pred. No. 1.1e+02;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 ggtacgcccgtacgctccgccc 23
 DB 1209 ggtacgcccgtccctccgccc 1187

Search completed: June 23, 2002, 15:09:02
 Job time: 78566 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2002, 06:31:50 / Search time 2161.72 seconds
(without alignments)

232,332 Million cell updates/sec

Title: US-09-747-514a-3

Sequence: 1 ccccttcggcgagcgagcgagcccg 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:*

- 1: gb-ba:*
- 2: gb-hgc:*
- 3: gb-in:*
- 4: gb-com:*
- 5: gb-act:*
- 6: gb-act:*
- 7: gb-ph:*
- 8: gb-pl:*
- 9: gb-pr:*
- 10: gb-ro:*
- 11: gb-sts:*
- 12: gb-sv:*
- 13: gb-sy:*
- 14: gb-vl:*
- 15: em-ba:*
- 16: em-fun:*
- 17: em-hum:*
- 18: em-in:*
- 19: em-mu:*
- 20: em-mu:*
- 21: em-or:*
- 22: em-ov:*
- 23: em-pat:*
- 24: em-ph:*
- 25: em-pl:*
- 26: em-ro:*
- 27: em-sts:*
- 28: em-vl:*
- 29: em-vl:*
- 30: em-hgc-hum:*
- 31: em-hgc-inv:*
- 32: em-hgc-other:*
- 33: em-hgc-inv:*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score actually printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description

C	1	24	100.0	3123	1	PAU83241	U83241 Pseudomonas
C	2	24	100.0	13075	1	AEO04946	AEO04946 Pseudomon
C	3	20.8	86.7	110000	2	LMFLOH16.E.03	Continuation (4 of
C	4	19.4	80.8	315000	1	RME6030444	AL6030444 Rhizobium
C	5	19.2	80.0	9000	1	SC9A10	AL031260 Streptomy
C	6	18.8	78.3	36877	9	AC005336	AC005336 Homo sapi
C	7	18.8	78.3	123653	9	AL162983	AL162983 Homo sapi
C	8	18.8	78.3	151764	9	AL162983	AL162983 Homo sapi
C	9	18.8	78.3	182433	2	AL358155	AL358155 Homo sapi
C	10	18.2	75.8	960	33	AC077474	AC077474 Giardia l
C	11	18.2	75.8	2214	5	AF045641	AF045641 Batbus ba
C	12	18.2	75.8	21057	3	LMF16751	LMF16751
C	13	18.2	75.8	43903	2	AC004425	AC004425 Homo sapi
C	14	18.2	75.8	65724	1	AF127374	AF127374 Streptom
C	15	18.2	75.8	121245	9	AC034240	AC034240 Homo sapl
C	16	18.2	75.8	163731	9	AC008949	AC008949 Homo sapl
C	17	17.8	74.2	434	11	G15956	G15956 human STS C
C	18	17.8	74.2	110000	2	LMFLOH36..33	Continuation (34 of
C	19	17.8	74.2	13289	2	AF004652	AF004652 Oryza sat
C	20	17.8	74.2	13289	2	AF004652	AF004652 Oryza sat
C	21	17.8	74.2	13289	2	AF004652	AF004652 Oryza sat
C	22	17.6	73.3	13771	33	AC039166	AC039166 Homo sapi
C	23	17.6	73.3	924	33	AC040499	AC040499 Giardia l
C	24	17.6	73.3	961	33	AC008938	AC008938 Giardia l
C	25	17.6	73.3	1449	1	CP165RMB	X73444 C.pnificum
C	26	17.6	73.3	2672	2	AF159692	AF159692 Myxococcu
C	27	17.6	73.3	4656	1	ECBBAACD	X87508 E.chrysanth
C	28	17.6	73.3	5241	1	HSSMA0251	U87126 Homo sapien
C	29	17.6	73.3	5241	1	HSSMA0251	U87126 Homo sapien
C	30	17.6	73.3	5241	1	HSSMA0251	U87126 Homo sapien
C	31	17.6	73.3	5869	1	AF111939	AF111939 Staphyloc
C	32	17.6	73.3	13409	1	AEO04466	AEO04466 Pseudom
C	33	17.6	73.3	13570	2	AC109008	AC109008 Rattus no
C	34	17.6	73.3	17864	2	AC068962	AC068962 Homo sapl
C	35	17.6	73.3	110000	2	AL607039..0	AL607039 Mus muscu
C	36	17.6	73.3	117004	2	AC108090	AC108090 Homo sapl
C	37	17.6	73.3	141706	9	AC010481	AC010481 Homo sapl
C	38	17.6	73.3	141894	9	AC009321	AC009321 Homo sapl
C	39	17.6	73.3	162839	2	AC106368	AC106368 Rattus no
C	40	17.6	73.3	164653	2	AC094444	AC094444 Rattus no
C	41	17.6	73.3	184777	9	AC026749	AC026749 Homo sapl
C	42	17.6	73.3	190008	1	AC094926	AC094926 Rattus no
C	43	17.6	73.3	340350	1	SM521791	AL521791 Shorthead
C	44	17.6	73.3	340350	1	SM521791	AL521791 Shorthead
C	45	17.6	73.3	340350	1	SM521791	AL521791 Shorthead

ALIGNMENTS

RESULT	1	3123 bp	DNA	linear	RCF 05-0CF-1996
LOCUS	PAU83241				
DEFINITION	Pseudomonas aeruginosa carboxate phosphotriphosyl transferase (pyrP),				
catabolite repression control protein (cro) and RNasePH (rph)					
genes, complete cds.					
ACCESSION	U83241				
VERSION	U83241.1				
KEYWORDS	U83241.1 GI:1079660				
SOURCE	Pseudomonas aeruginosa strain PAO1.				
ORGANISM	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;				
REFERENCE	1 (bases 1 to 3123)				
AUTHORS	McGregor, C.H., Arora, S.K., Hager, P.W., Dall, M.B. and Phillips, P.V.				
TITLE	UT nucleotide sequence of the Pseudomonas aeruginosa pyrP-crc-rph				
JOURNAL	J. bacteriol. 178 (19), 5627-5635 (1996)				
MEDLINE	96421989				
REFERENCE	2 (bases 1 to 3123)				
AUTHORS	Hager, P.W. and Phillips, P.V. Jr.				
TITLE	Direct Submission				

DB 6644 CC8CTCGGGCGGAGCAAGACCCGG 6621

RESULT 6
AC005336 36874 bp DNA linear P1 15-JUN-2001
LOCUS Homo sapien chromosome 19, cosmid F20129, complete sequence.
DEFINITION
AC005336
VERSION
AC005336.1 GI:3347821
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 36874)
Burkhardt, J.E., McCreedy, P.M., Skowronski, E., Adamson, A.W.,
Lamerdin, J.E., Gordon, L., Kyle, A., Ramirez, M., Stilaugen, S.,
Regala, M., Do, L., Regala, M., Terry, A., Gaines, J.,
Dunne, J., Christensen, M., Georges, A., Ayala, J.,
Liu, S., Altis, C., Andrieux, R., Truitt, B., Thomas, P.,
Coffield, J., Darter, S., Lucas, S., Bruce, P., Thomas, P.,
Krommiller, B., Ariellano, A., Montgomerie, M., Or, D., Nolan, M.,
Tromb, S., Kobayashi, A., Olson, A.S. and Carrano, A.V.
Sequence analysis of a 1.5 Mb OLFR-rich region in 19p13.1
Genomics 43:1-12 (2001)
2 (bases 1 to 36874)
Lamerdin, J.E.
Direct Submission
Submitted (29-JUL-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Map and sequence oriented from p teletome to centromere. Cosmid
F20129 overlaps cosmid R26420 (AC004791) to the left from bases 1
to 723 and cosmid R26420 overlaps cosmid R28342 to the right by
approx. 6 kb. Additional mapping information are available
at: <http://www.bio.lbl.gov/bjrrp/genome/genome.html>.

FEATURES
source
1. 36874
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19p13.1 from OLFR to MEL"
/clone="F20129"
/cell_line="UV5H9-59"
/clone_id="UV5H9-59"
/note="Cosmid library constructed at LNL from flow-sorted
chromosomes from human hamster hybrid UV5H9-59, which
contains chromosome 19 as its only human chromosome."
190..362
/note="BDS similarity to M377259 ESTP9796. Small intestine
II Homo sapiens cDNA 3' end similar to cytochrome P450,
subfamily 1F, polypeptide 2; Score: 334 identity:
170/173 (98%)."
170/173 (98%).
complement(260..20308)
P1 clone from cytochrome P450 4F2 (CYP4F2) mRNA
complement(1363..3535)
/rpt_family="L1M65"
complement(1007..19847)
/gene="CYP4F2"
/note="cytochrome P450 4F2"
complement(1007..1172,1582..1664,1840..1904,
20308..21109..6285,6478..8344,11659..11929,
12548..12669,14543..14672,14783..14818,17742..17886,
19650..19847)
/gene="CYP4F2"
/note="cytochrome P450 4F2; leukotriene B4
omega-hydroxylase; LEUKOTRIENE-B4 20-MONOOXYGENASE;
OTOCORHONE P450-17B-OMEGA; LEUKOTRIENE-B4
Oxidase; HDMOXILASE"
evidence=not_experimental
/product="CYP4F2"
/protein_id="AAC27730.1"
/db_xref="GI:3347822"

repeat_region
2583..2871
/rpt_family="A1u9"
repeat_region
3149..3382
/rpt_family="L1M02"
repeat_region
3239..3382
/rpt_family="L1M07"
repeat_region
3600..3711
/rpt_family="L1M47"
repeat_region
3712..3841
/rpt_family="T6A0a.n"
repeat_region
4000..4138
/rpt_family="T6A0a.n"
repeat_region
4139..4500
/rpt_family="L1M47"
repeat_region
4515..4818
/rpt_family="A1u9g"
repeat_region
4818..4962
/rpt_family="L1M47"
repeat_region
5285..6013
/rpt_family="L1M47"
repeat_region
6015..6314
/rpt_family="A1u9g"
repeat_region
6317..6350
/rpt_family="GA)n"
repeat_region
6359..6866
/rpt_family="L1M47"
repeat_region
7018..7328
/rpt_family="L1M47"
repeat_region
complement(7730..7392)
/rpt_family="GA)n"
repeat_region
complement(9042..9092)
/rpt_family="GA)n"
repeat_region
9278..9310
/rpt_family="CA)n"
repeat_region
9544..9678
/rpt_family="CA)n"
repeat_region
9985..10104
/rpt_family="CA)n"
repeat_region
10176..10222
/rpt_family="CA)n"
repeat_region
10383..10412
/rpt_family="CA)n"
repeat_region
10550..10668
/rpt_family="CA)n"
repeat_region
10670..10744
/rpt_family="CA)n"
repeat_region
10746..10916
/rpt_family="CA)n"
repeat_region
10919..11035
/rpt_family="CA)n"
repeat_region
12968..13227
/rpt_family="CA)n"
repeat_region
complement(14390..14462)
/rpt_family="A1R"
repeat_region
complement(14533)
/rpt_family="A1R"
repeat_region
17916..17998
/rpt_family="A1R"
repeat_region
complement(18011..18148)
/rpt_family="T6A0a.n"
repeat_region
complement(18159..18379)
/rpt_family="T6A0a.n"
repeat_region
complement(18372..18512)

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the overlapping clone name may not be found in the sequence submission corresponding to the difference as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30): an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one compression and repeat; the restriction site structure and the assembly was confirmed by restriction digest and sequencing. Given the feature table with their source databases: Em, EMBL, SW, SWISSPROT, Tr, TrEMBL, Wp, WormPeP, information on the WormPeP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was constructed by the International Clone Contigs of Human Mapping Group. Further information can be found at <http://www.sanger.ac.uk/hcg/chr13> RPI1-36362 is from the library RPI1-11.2 constructed by the group of Plietzer de Jong. For further details see <http://www.chori.org/dacpac/home.htm>

FEATURES

SOURCE

IMPORTANT: This sequence is not the entire insert of clone RPI1-36362. It may be shorter because we sequenced overlapping sections only once, except for a 100 base overlap. The true left end of clone RPI1-124M19 is at 123594 in this sequence. The true right end of clone RPI1-274P12 is at 100 in this sequence.

```

location=Qualifiers
1..123594
db_xref=taxon:9606
/organism="Homo sapiens"
/chromosome="13"
/clone="RPI1-36362"
/clone_1bp="RPI1-11.2"
146..445
/note="146-445 repeat: matches 1..310 of consensus"
repeat_region
1159..1208
/note="1159-1208 repeat: matches 2 mer tt 744 conserved"
repeat_region
1738..2031
/note="1738-2031 repeat: matches 11..306 of consensus"
repeat_region
2845..2890
/note="2845-2890 repeat: matches 1..306 of consensus"
repeat_region
3907..4053
/note="3907-4053 repeat: matches 21..176 of consensus"
repeat_region
4765..5022
/note="4765-5022 repeat: matches 21..176 of consensus"
repeat_region
5459..5752
/note="5459-5752 repeat: matches 21..176 of consensus"
repeat_region
5763..5869
/note="5763-5869 repeat: matches 1..293 of consensus"
repeat_region
5905..5982
/note="5905-5982 repeat: matches 6004..6110 of consensus"
repeat_region
6150..6910
/note="6150-6910 repeat: matches 161..226 of consensus"
repeat_region
7127..7404
/note="7127-7404 repeat: matches 274..1752 of consensus"
repeat_region
7652..7748
/note="7652-7748 repeat: matches 1..281 of consensus"
repeat_region
7805..8031
/note="7805-8031 repeat: matches 2600..2702 of consensus"
repeat_region
10436..11460
/note="10436-11460 repeat: matches 21..204 of consensus"
repeat_region
12866..13180
/note="12866-13180 repeat: matches 1410..2698 of consensus"
repeat_region
13593..13628
/note="13593-13628 repeat: matches 1..312 of consensus"
repeat_region
13858..14022
/note="13858-14022 repeat: matches 2 mer gt 866 conserved"
repeat_region
14055..15099
/note="14055-15099 repeat: matches 77..248 of consensus"

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repeat_region
14055..15099
/note="14055-15099 repeat: matches 4378..5361 of consensus"
repeat_region
15040..15406
/note="15040-15406 repeat: matches 1..369 of consensus"
repeat_region
15407..15722
/note="15407-15722 repeat: matches 5361..6241 of consensus"
repeat_region
15723..16300
/note="15723-16300 repeat: matches 2 mer tg 964 conserved"
repeat_region
16325..16433
/note="16325-16433 repeat: matches 6239..6326 of consensus"
repeat_region
16397..16799
/note="16397-16799 repeat: matches 5297..5709 of consensus"
repeat_region
16800..17112
/note="16800-17112 repeat: matches 1..308 of consensus"
repeat_region
17113..17555
/note="17113-17555 repeat: matches 5709..6129 of consensus"
repeat_region
17666..17956
/note="17666-17956 repeat: matches 1..297 of consensus"
repeat_region
18501..18815
/note="18501-18815 repeat: matches 1..307 of consensus"
repeat_region
18860..19482
/note="18860-19482 repeat: matches 4857..5765 of consensus"
repeat_region
19843..20151
/note="19843-20151 repeat: matches 1..309 of consensus"
repeat_region
20152..20466
/note="20152-20466 repeat: matches 5769..6088 of consensus"
repeat_region
20975..21271
/note="20975-21271 repeat: matches 1..299 of consensus"
repeat_region
21272..21584
/note="21272-21584 repeat: matches 5..297 of consensus"
repeat_region
21918..22218
/note="21918-22218 repeat: matches 7..307 of consensus"
repeat_region
22560..22654
/note="22560-22654 repeat: matches 217..311 of consensus"
repeat_region
22655..22879
/note="22655-22879 repeat: matches 5752..6173 of consensus"
repeat_region
27823..27886
/note="27823-27886 repeat: matches 5404..5722 of consensus"
repeat_region
28146..28511
/note="28146-28511 repeat: matches 2679..2741 of consensus"
repeat_region
28603..29011
/note="28603-29011 repeat: matches 1572..1949 of consensus"
repeat_region
30976..31289
/note="30976-31289 repeat: matches 3..460 of consensus"
repeat_region
31350..31405
/note="31350-31405 repeat: matches 1..312 of consensus"
repeat_region
31589..31854
/note="31589-31854 repeat: matches 28 copies 2 mer on 694 conserved"
repeat_region
32300..32416
/note="32300-32416 repeat: matches 1..285 of consensus"
repeat_region
33065..33222
/note="33065-33222 repeat: matches 5625..5750 of consensus"
repeat_region
33577..33688
/note="33577-33688 repeat: matches 2540..2710 of consensus"
repeat_region
33960..34166
/note="33960-34166 repeat: matches 1760..1771 of consensus"
repeat_region
34167..34178
/note="34167-34178 repeat: matches 697..914 of consensus"
repeat_region
34290..34535
/note="34290-34535 repeat: matches 1771..2002 of consensus"
repeat_region
34639..34700
/note="34639-34700 repeat: matches 5321..5558 of consensus"
repeat_region
34758..34851
/note="34758-34851 repeat: matches 506..574 of consensus"
repeat_region
34852..35438
/note="34852-35438 repeat: matches 6136..6229 of consensus"
repeat_region
35439..36300
/note="35439-36300 repeat: matches 5585..6157 of consensus"

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misc_feature /note="11A7 repeat: matches 5273. 6137 of consensus"
37701..38100
misc_feature /note="match: GSS: Em:A0152136"
38805..38904
misc_feature /note="match: GSS: Bm:A0197787"
39078..39087
misc_feature /note="match: GSS: Bm:A0793043"
39086..39285
repeat_region /note="AluSc repeat: matches 1. .280 of consensus"
39322..39636
repeat_region /note="AluSp repeat: matches 1. .313 of consensus"
39657..39716
repeat_region /note="AluSc repeat: matches 57. .115 of consensus"
40025..41021
repeat_region /note="L1R33 repeat: matches 1. .151 of consensus"
41075..41201
repeat_region /note="AluB repeat: matches 170. .296 of consensus"
41202..41429
repeat_region /note="L1R1 repeat: matches 225. .492 of consensus"
41430..41653
repeat_region /note="AluJ7 repeat: matches 1. .220 of consensus"
41654..41777
repeat_region /note="L1M4 repeat: matches 4511. .4735 of consensus"
41738..42963
repeat_region /note="L1M4 repeat: matches 5042. .6290 of consensus"
42966..44070
repeat_region /note="L1M3 repeat: matches 4694. .5818 of consensus"
44071..44246
repeat_region /note="L1M3 repeat: matches 142. .311 of consensus"
44246..44577
repeat_region /note="AluSp repeat: matches 1. .312 of consensus"
44578..44716
repeat_region /note="AluSc repeat: matches 1. .142 of consensus"
44717..44845
repeat_region /note="L1M5 repeat: matches 5818. .6059 of consensus"
44851..45153
repeat_region /note="L1P13 repeat: matches 5293. .6154 of consensus"
45154..45383

Query Match 78.3% Score 18.8; DB 9; Length 123693;
Best Local Similarity 90.9%; Pred. No. 5.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 gttcggcgcgaagaagccgg 24
DB 73573 GCTCGGCGCGAGAGCCCG 73594

```

```

REFERENCE 4 (bases 1 to 151764)
AUTHORS Smith,D.R.
DIRECT SUBMISSION
TITLE Direct Submission (09-JUN-2001) Genome Therapeutics Corporation, 100 Beaver
JOURNAL JOURNAL
COMMENT On May 7, 2000 this sequence version replaced g1:6310512.
FEATURES
source
1..151764
/organism="Homo sapiens"
/db_xref="taxid:9606"
/collection="RP11-179B15"
/clone_id="RP11-179B15"
BASE COUNT 47476 a 29555 c 29458 g 45274 t 1 others
ORIGIN

Query Match 78.3% Score 18.8; DB 9; Length 151764;
Best Local Similarity 90.9%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 gttcggcgcgaagaagccgg 24
DB 69869 GCTCGGCGCGAGAGCCCG 69890

RESULT 10
AL358155 182433 bp DNA linear HTG 10-JUL-2001
LOCUS Homo sapiens chromosome 10 clone RP11-637J22, ** SEQUENCING IN
DEFINITION
ACCESSION AL358155.17 GI:14529817
VERSION AL358155.17
KEYWORDS HTG; RP11-637J22; HTG-CANCELLED.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 182433)
REFERENCE Williams,S.
AUTHORS
TITLE Direct Submission (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL CBIO 15N, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Jun 22, 2001 this sequence version replaced g1:14348459.
COMMENT
----- Genome Center
Center: Sanger Centre
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
Project Information
Center project name: DAB37J22
Summary Statistics
Sequencing program: XCAP4; version 4.5
Sequencing vector: pBluescript II-Dx2; 100% of reads
Chemical modification: None; 100% of reads
Consensus quality: 182127 bases at least Q40
Consensus quality: 182344 bases at least Q30
Consensus quality: 182368 bases at least Q20
Insert size: 182433; sum-of-contigs
Insert size: 201690; 10-2% error; agarose-fp
Quality coverage: 7-30x in Q20 bases; sum-of-contigs Quality
coverage: 6-60x in Q20 bases; agarose-fp
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
1..182433 "Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxid:9606"
/chromosome="10"

```


DEFINITION	AL135896	AL135896.1	GI:6635092	multitiding resistance protein, copy 1; multitiding resistance protein, copy 2
VERSION	1			
KEYWORDS				
SOURCE	Leishmania major.			
ORGANISM	Leishmania major.			
REFERENCE	1 (bases 1 to 21057)			
AUTHORS	Ivans A.C., Lewis S.M., Boghevaraden A., Zhang L., Chan H.M. and			
TITLE	Smith D.R. map of the Leishmania major Friedlin genome			
JOURNAL	Genome Res. 8 (2), 135-145 (1998)			
MEDLINE	98146435			
REFERENCE	2 (bases 1 to 21057)			
AUTHORS	Zimmerman M., Mamblut R., Ivans A.C., Murphy L., Quall M.,			
TITLE	Rejzndrean M.A. and Barrell B.G.			
JOURNAL	Submitted (22-Dec-1999) European Leishmania major Friedlin genome			
MEDLINE	98146435			
REFERENCE	3 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	4 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	5 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	6 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	7 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	8 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	9 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	10 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	11 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	12 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	13 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
MEDLINE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
REFERENCE	14 (bases 1 to 21057)			
AUTHORS	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
TITLE	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			
JOURNAL	Smith D.R., Smith S.E., Smith S.E., Smith S.E., Smith S.E., Smith S.E.,			

OM nucleic - nucleic search, using SW model

63.187 Million cell updates/sec

Sequence: 1 ccgttcgagcgaggaagcccg 24

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters:	3472872
--	---------

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_032802:*.

1. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1380.DAT
2. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1381.DAT
3. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1382.DAT
4. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1383.DAT
5. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1384.DAT
6. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1385.DAT
7. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1386.DAT
8. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1387.DAT
9. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1388.DAT
10. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1389.DAT
11. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1390.DAT
12. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1391.DAT
13. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1392.DAT
14. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1393.DAT
15. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1394.DAT
16. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1395.DAT
17. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1396.DAT
18. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1397.DAT
19. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1398.DAT
20. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1399.DAT
21. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1400.DAT
22. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1401.DAT
23. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1402.DAT
24. /net/abss06/s1d51/gcgdata/hold_genesec/genesec_embd/VNA1403.DAT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.8	78.3	1241	AA187016	human polyomavirus
2	18.2	75.8	1413	AA658017	human polyomavirus
3	18.2	75.8	1413	AA658017	Complete nucleotide
4	18.2	75.8	53500	AA658042	U143 homologous gen
5	17.4	72.5	1496	AA078155	Nucleotide sequenc
6	17.4	72.5	1499	AA653158	RNA encoding bovin
7	17.4	72.5	1499	AA653158	RNA encoding bovin
8	17.4	72.5	12749	AA673032	U143 homologous ge
9	17.2	71.7	48275	AA481501	U143 homologous ge
10	17.2	71.7	349980	AA621610	U143 homologous ge

[illegible]

PI Sherman DH, Mao Y, Varoglu M, He M, Sheldon PC:
 XX WPI: 2000-601980/57.
 OR Novel nucleic acid molecule comprising mitomycin biosynthetic gene
 XX cluster useful for cloning mitomycin biosynthetic genes for elucidating
 XX the molecular basis of mitomycin ring system biosynthesis -
 XX Disclosure: Figure 26; 399pp: English.

CC This invention relates to isolated and purified nucleic acid molecules
 CC comprising a mitomycin biosynthetic gene cluster. Mitomycins are a group of
 CC natural products that have been shown to have a variety of biological
 CC amino benzoxazinone and oxiridine ring systems. Mitomycins are
 CC mitomycin biosynthetic gene cluster comprises 47 mitomycin genes
 CC spanning 55kb of DNA. The invention includes an expression cassette
 CC comprising a mitomycin biosynthetic gene operably linked to a promoter,
 CC and host cells transformed with the cassette. The nucleotide, and protein
 CC and the transformed host cells of the invention result in
 CC antibiotic activities. The nucleotide, and protein
 CC as to engineer the biosynthesis of novel natural products, e.g.
 CC as to engineer the biosynthesis of novel natural products, e.g.
 CC antibiotics, anti-inflammatory agents, anti-cancer agents,
 CC immunoenhancers, immunosuppressants, agents to treat asthma, chronic
 CC respiratory disease as well as other disease involving
 CC protective agents (e.g. fungicides, herbicides, lowering agents or as crop
 CC protection agents) in packaging or biomedical applications, as well as
 CC polymers, e.g., in packaging or biomedical applications, as well as
 CC PNA monomer syntheses. Sequences AAC55782-C55881, AAC55815-C55869 and
 CC AAC37485-B32542 represent mitomycin biosynthetic gene cluster DNA
 CC sequences and encoded proteins. Sequences AAC55812-C55814,
 CC AAC35850-C55836 and AAC35862-C55869 represent PCR primers used in the
 CC cloning of the mitomycin biosynthetic genes.

SO Sequence 53500 BP: 7481 A; 19740 C; 19126 G; 7153 T; 0 other:

Query Match
 Best Local Similarity 75.8%; Score 18.2; DB 21; Length 53500;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 CGCTCGGCGCGAGGAGCGG 23
 Db 24533 CAGTTCGCGCGAGGAGCGG 24511

RESULT 4
 ID AA078165 standard: DNA; 1496 BP.
 XX AA078165;
 AC
 XX 07-JUN-1995 (first entry)
 DT
 XX U149 homologue gene of bovine herpes virus 1 (BHV-1).
 DE
 XX Cattle pathogen: Infectious bovine rhinotracheitis; nucleocapsid.
 KW
 VPI; promoter: ss.
 RM
 XX Bovine herpes virus 1.
 OS
 XX Key
 XX Location/Qualifiers
 FT CDS
 FT /tag= a
 FT /label= dnpase (U150) ORF start codon
 FT 1..266
 FT /tag= b
 FT /label= U149.5 gene
 FT 236..258
 FT 294..300
 FT TATA_signal
 FT /tag= d

FT RBS 333..335
 FT /tag= e
 FT polyA_signal 1226..1231
 FT /tag= f
 FT CDS 1351..1496
 FT /tag= g
 FT /label= U148 ORF

PH W09424296-A.
 XX 27-OCT-1994.
 PD
 XX
 XX 19-APR-1994; 94MO-CM0201.
 PF
 XX 19-APR-1993; 93US-0051448.
 XX (UWSA-) UNIV SASKATCHEWAN.
 FA
 XX Liang X, Rabulk LA, Zamb T;
 P1
 WPI: 1994-241875/42.
 DR P-508; AAR63461.
 XX
 XX Mutant bovine herpes type 1 virus with deleted gene(s) - used as
 FT vaccine, also with replacement bacterial or viral pathogen
 FT immunogens and/or cytokine(s), inserted at deletion

PS Example: Fig 11; 109pp: English.

CC AA078165/63461 are the nucleotide sequence and deduced AA sequence
 CC of BHV 1 U149 homologue gene. The AA sequence deduced from the
 CC U148 homologue gene and dnpase gene (U150 homologue gene) are
 CC presented. Putative G-C box, TATA box and polyA signal sequence
 CC are indicated in FT. The boundaries of U150, U149.5 and U148
 CC ORFs surrounding the U149 homologue gene are also indicated.

SO Sequence 1496 BP: 212 A; 535 C; 517 G; 232 T; 0 other:

Query Match
 Best Local Similarity 72.5%; Score 17.4; DB 15; Length 1496;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 6 CGGCGCGAGGAGCGG 24
 Db 695 CGGCGCGAGGAGCGG 677

RESULT 5
 ID AAAS9128/6
 XX AAAS9128 standard: DNA; 1499 BP.
 AC
 XX AAAS9128;
 AC
 XX 07-NOV-2000 (first entry)
 DT
 XX Nucleotide sequence of the U149 gene homologue of BHV-1.
 DE
 XX U149, homologue: Bovine herpesvirus 1; BHV-1; attenuated virus;
 KW essential gene; BHV-1 infection; vaccine; cattle; ss.
 RM
 XX Bovine herpesvirus.
 OS
 XX Key
 XX Location/Qualifiers
 FT CDS
 FT 390..1166
 FT /tag= a
 FT /product= "U149 homologue"
 PN US6086902-A.
 XX 11-JUL-2000.
 PD
 XX 09-SEP-1994; 94US-0303861.

XX	PR	19-APR-1993:	9305-0051448.
XX	XX	(UYSA-) UNIV SASKATCHEWAN.	
XX	PI	Babluik LA, Zamb T, Liang X:	
XX	DR	WPIJ. 2000-531337/48.	
XX	DR	P-PSDB: AAB07662.	
XX	XX	Immunogenic composition useful as vaccine against herpesvirus infection	
XX	PT	in domestic ruminants comprising a mutation	
XX	PT	in at least one essential gene to reduce its virulence	
XX	XX	Example 15: Fig 11: 56pp: English.	
XX	XX	The present sequence encodes a Bovine herpesvirus 1 (BHV-1) UIA9	
XX	CC	gene homologue polypeptide. The gene was altered to create the viruses	
XX	CC	of the invention. The specification describes an immunogenic composition	
XX	CC	comprising essential elements of wild type BHV-1 to reduce the in at	
XX	CC	virulence of the virus. The immunogenic composition is useful for	
XX	CC	treating or preventing BHV-1 infection in a bovine host. It is also	
XX	CC	useful as vaccine to immunize cattle against infection with wild	
XX	CC	type BHV-1.	
XX	XX	Sequence 1499 BP: 212 A: 536 C: 519 G: 232 T: 0 other:	
XX	XX	Query Match 72.5%: Score 17.4: DB 21: Length 1499:	
XX	XX	Best Local Similarity 94.7%: Pred. No. 1.4e-02:	
XX	XX	Matches 18: Conservative 0: Mismatches 1: Indels 0: Gaps 0:	
XX	XX	6 cgggcgcgagagaccgcg 24	
XX	XX		
XX	XX	695 cgcgcgcgcgcgcgcgcgc 677	
XX	XX		
XX	XX	RESULT 6	
XX	XX	AA518163/O	
XX	ID	AA518163 standard: DNA: 1499 BP.	
XX	XX	AA518163:	
XX	XX	26-MAR-2002 (first entry)	
XX	DE	DNA encoding bovine herpesvirus protein.	
XX	XX	Bovine herpesvirus protein: gene therapy; reporter protein; ds.	
XX	XX	Bovine herpesvirus 1.	
XX	XX	Location/Qualifiers	
XX	XX	Key 390..1165	
XX	XX	CDS /'cseg' a	
XX	XX	FT /product= "Bovine herpesvirus protein"	
XX	XX	US6316252-B1.	
XX	XX	13-NOV-2001.	
XX	XX	17-DEC-1998: 98US-0213343.	
XX	XX	17-DEC-1998: 98US-0213343.	
XX	XX	(MISC) WISCONSIN ALUMNI RES FOUND.	
XX	XX	harme JS, Splitter GA:	
XX	XX	WPI: 2002-074374/10.	
XX	XX	P-PSDB: AAU11367.	
XX	XX	New bovine herpes virus protein linked to a non-bovine reporter	

PT	protein useful for delivering therapeutic and/or reporter proteins to mammalian cells, either in vitro or in vivo
XX	
XX	Example 2; Column 5-8; bpg: English.
CC	The invention relates to a peptide comprising bovine herpesvirus protein linked to a non-bovinate reporter protein. The peptide is useful for delivering therapeutic and/or reporter proteins to mammalian cells, either in vitro or in vivo. It is especially suited to deliver proteins to ruminant and primate cells, thus has in vivo and in vitro pharmaceutical, veterinary and research applications. The system permits delivery of effector proteins deep within tissues. This system also represents DNA encoding the bovine herpesvirus protein of the invention.
XX	
XX	
S0	Sequence 1499 BP; 212 A; 536 C; 519 G; 232 T; 0 other;
Query Match	72.5% ; Score 17.4 ; DB 24; Length 1499;
Best Local Similarity	94.7% ; Pred. No. 1.4e+02;
Mechanism	18; Conservative; Mismatches 0; Indels 0; Gaps 0
Dy	6 CGGCGCGAGGAAGCGCG 24 695 CGGGCGCAGACGCGCG 677
RESULT 7	
AAKY78032.7	
T	AAKY78032 standard; cDNA to mRNA; 12749 BP.
AC	AAKY78032:
DT	19-AUG-1999 (first entry)
XX	
DE	Human Huntington's chorea associated protein homologue cDNA.
KM	Huntington's chorea; human; model; db.
OS	Homo sapiens.
FN	
FT	JPI137258-A.
PD	25-MAY-1999.
XX	
XX	14-NOV-1997; 97Jp-0314020.
PR	14-NOV-1997; 97Jp-0314020.
XA	(SLAF-) SLA KENKUYSHO KR.
XX	
DR	WPI: 1999-374378/32.
P-RSDb:	NAF08896.
CC	cDNA of Huntington's gene - useful for development of animal model of Huntington's disease
PT	
PT	Claim 1; Page 6-10; 18pp: Japanese.
PS	
CC	This invention describes a novel human Huntingtin's chorea associated protein homologue. The development of a model animal of Huntington's disease are useful for the development of a model animal of Huntington's disease
XX	
XX	Sequence 12749 BP; 2292 A; 4064 C; 3925 G; 2468 T; 0 other;
Query Match	72.5% ; Score 17.4 ; DB 20; Length 12749;
Best Local Similarity	94.7% ; Pred.No. 1.3e+02;

Query Match	Best Local Similarity	81.74%	Score 17.2	DB 21:	Length 4875;
Matches 19;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0	
2	cgctggcgcgcggaagacgcg	23			
Db 27591	cgctggcgcggaagacgcg	27612			
RESULT 9	AAFP21610/C				
ID	AAFP21610 standard: DNA; 349980 BP.				
XX	AAFP21610.				
DE	13-MAR-2001 (first entry)				
DE	Neisseria meningitidis B nucleotide sequence SEQ ID NO.111.				
XX	Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;				
XX	diagnosis; antigen; detection; infection; gene therapy; antibacterial;				
XX	ds.				
XX	Neisseria meningitidis.				
XX	MO200066791-AL.				
XX	08-NOV-2000.				
XX	08-MAR-2000; 2000MO-US05928.				
XX	30-APR-1999; 99US-0132068.				
XX	08-OCT-1999; 99MO-US23573.				
XX	28-FEB-2000; 2000CB-0004655.				
XX	(CHIR) CHIRON CORP.				
XX	(GENO-) INST GENOMIC RES.				
XX	Pizza M, Hickley P, Patterson J, Tettelin R, Venter JC, Masignani V;				
XX	Galorini C, Morri M, Ratti G, Scarselli M, Scarlato V, Masignani V;				
XX	Frazer CM, Grand G;				
XX	WPI: 2000-647603.62.				
XX	Neisseria meningitidis B full length genome sequence and open reading				
XX	frames are used to detect, treat and prevent Neisserial infections -				
XX	Claim 7; Appendix A: 692pp: English.				

XX Sequence 34980 BP: 86771 A; 92803 C; 86340 G; 84066 T; 0 other:
 SQ
 Query Match 71.7%: Score 17.2; DB 21; Length 34980;
 Best Local Similarity 86.4%; Pred. No. 4e+02;
 Matches 19: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 2 cgttcgagcgagagagagccgc 23
 |||||
 DB 297563 CGTTCGCGCAGCAGAACCCGC 297542

RESULT 10
 ID AAO20907 standard; DNA, 9431 BP.
 XX AAO20907;
 AC
 XX 22-MAY-1992 (first entry)
 DT
 XX DNA encoding the chimeric protein V1V2-HC2-KA.
 XX
 XX CD4, LTR: Streptomyces longisporus; HIV gp120; AIDS; IgG1; T cell;
 KW Immunoglobulin; surface glycoprotein; virus; MHC class II; ss.
 XX
 OS Homo sapiens.
 XX Key Location/Qualifiers
 XX signal_peptide 648..731
 FT //tag= a
 FT met_peptide 732..1286
 FT //tag= b
 FT misc_feature 1287..1331
 FT //function= hinge_region
 FT 1332..1680
 FT met_peptide
 FT //tag= d
 FT //product= CH2

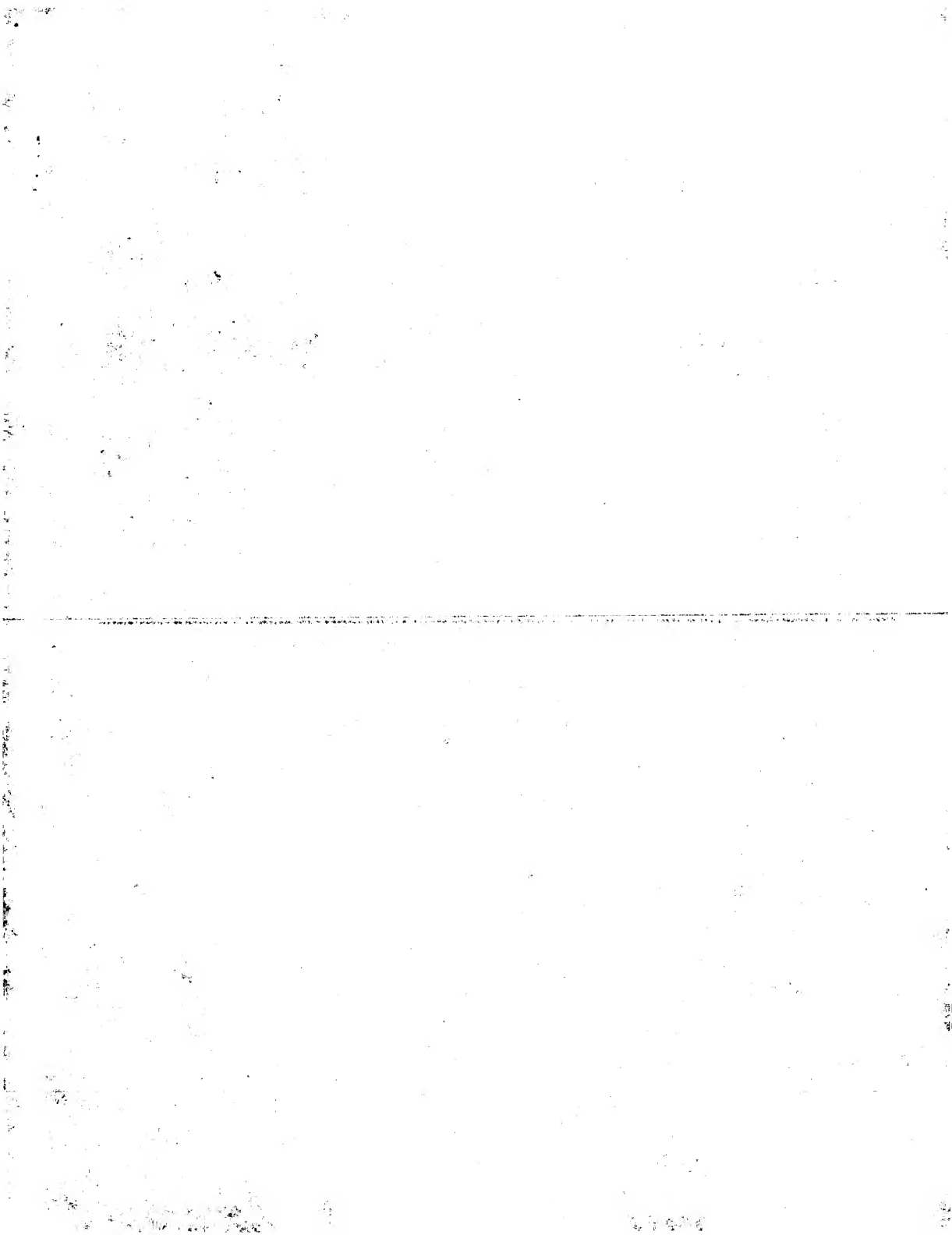
XX MO9200985-A.
 XX 23-JAN-1992.
 XX 01-JUL-1991; 91NO-US04663.
 XX
 XX 05-MAR-1991; 91US-0665218.
 PR 11-JUL-1990; 90US-0551584.
 XX (SNIK) SMITHKLINE BEECHAM.
 XX
 PI Brauner ME, Fornwald JA, Arthos J;
 PI
 XX WPI: 1992-056814/07.
 DR P-PSDB, AAR20634.
 DR
 XX Nucleic acid sequences for production of CD4 chimeric protein -
 PT used to transfect streptomyces, contg. LTR signal sequence linked
 PT to pro-peptide sequence facilitating peptide cleavage
 XX
 PS Claim 10; Page 23; 47pp; English.
 PS
 XX The sequence was obt'd. by sequencing the plasmid vector V1V2-HC2-KA.
 CC Plasmid 112-nucleotide SV40 origin, SV40 origin, SV40 origin, SV40 origin,
 CC Plasmid construct contains a CD4 chimera (V1V2) in which the
 CC carboxy terminal portion of the encoded protein consists of a murine
 CC immunoglobulin light chain constant region. This sequence is
 CC operably linked to the coding sequence of the signal peptide of
 CC streptomyces LTR, modified at its 5' end by the addition of bases
 CC encoding lys-Arg. Also included in the expression vector is the
 CC sequence encoding an 1901 constant region comprising the hinge and

CC CH2 motifs. Human IgG1 is the most effective immunoglobulin
 CC subclass at mediating cell killing by both complement and ADCC.
 CC The vectors are used for the prom. of 301 binding region. It is joined
 CC in bacterial host, the human Ig constant region lacking the CH3 domain,
 CC which increases the stability of the CD4, thus increasing the serum
 CC half life and/or potency against HIV infection and inhibit
 CC virus-induced cell fusion, relative to soluble CD4.
 CC See also AAO20908.9.
 CC
 XX
 SQ Sequence 9431 BP: 1712 A; 2938 C; 2964 G; 1808 T; 9 other:
 XX
 Query Match 70.0%: Score 16.8; DB 13; Length 9431;
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;
 Matches 18: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 2 cgttcgagcgagagagagccgc 21
 |||||
 DB 4836 cgttcgagcgagagagagccgc 4835

RESULT 11
 ID AAR29361/C standard; DNA, 85 BP.
 XX AAR29361;
 XX
 XX 17-JUL-2001 (first entry)
 DT
 XX Drosophila melanogaster essential gene fragment, SEQ ID NO: 550.
 DE
 XX Drosophila melanogaster; fruit fly; essential gene; screening assay;
 KW pesticide; crop protection; chromosome 3; ds.
 XX
 XX Drosophila melanogaster.
 OS
 XX NO200118547-A1.
 PN
 XX 15-MAR-2001.
 PD
 XX 06-SEP-2000; 2000NO-GB03444.
 XX
 XX 07-SEP-1999; 99GB-0021009.
 PR
 XX (UNITU) UNITU GLASGOW.
 PA
 XX Davies RM, Kaiser K, Yang MW;
 PI
 XX WPI: 2001-281436/29.
 DR
 XX
 PT Screening assays for used for identifying compounds having a
 PT physiological effect on proteins identified as being essential -
 PT
 XX Claim 23; Page 483; 695pp; English.
 PS
 XX The present sequence is part of an essential gene from Drosophila
 CC melanogaster. Lack of expression of the protein encoded by this
 CC gene leads to a lethal or semi-lethal phenotype. The invention
 CC relates to 902 nucleic acid sequences from genes encoding proteins
 CC which are thought to be essential, and to a screening assay these
 CC identifying compounds which are useful as pesticides and may be used
 CC products. Such compounds are useful as pesticides and may be used
 CC protection with other pesticides and herbicides for crop
 CC protection. The gene corresponding to the present sequence is located
 CC on chromosome 3.
 CC
 XX
 SQ Sequence 85 BP: 27 A; 19 C; 24 G; 15 T; 0 other:
 XX
 Query Match 69.2%: Score 16.6; DB 22; Length 85;
 Best Local Similarity 82.6%; Pred. No. 3.3e+02;
 Matches 19: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

C C AAS44946;
 X T 18-DEC-2001 (first entry)
 X X cDNA encoding novel human secretory protein, Seq ID No. 27.
 X X Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 X X ischemia-reperfusion injury; haemophagocytosis; cancer; neutropathy;
 X X transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 X X myotrophic lateral sclerosis; platelet disorder; thrombocytopata;
 X X ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 X X gut protection; lung; liver fibrosis; immune deficit disorder; allergy;
 X X multiple sclerosis; Crohn's disease; arthritis; diabetes mellitus; asthma;
 X X fertility; analgesic; pain; antigen; ss.
 X S Homo sapiens.
 X X
 X X W0200166689-A2.
 X X
 X X 13-SEP-2001.
 X X
 X X 05-MAR-2001; 2001MO-US04942.
 X X
 X X 07-MAR-2000; 2000US-051970S;
 X X 17-MAY-2000; 2000US-057445A;
 X X 19-JUN-2000; 2000US-0596193;
 X X 14-JUL-2000; 2000US-0616847;
 X X 16-SEP-2000; 2000US-0653563;
 X X 20-OCT-2000; 2000US-0693267.
 X X
 X X (HSE-) HYSDO INC.
 X X
 X X Tang YF, Liu C, Asundi V, Xu C, Wehman T, Ren F, Ma Y, Zhou P,
 X X Zhao QX, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 X X P-FSDB: AN028046.
 X X WPI: 2001-589934/56.
 X X
 X X Novel polypeptides and nucleic acids obtained from cDNA libraries
 X X prepared from various human tissues, for diagnosis and treatment of
 X X cancer, neurological, inflammatory, and autoimmune disorders -
 X X
 X X Claim 1: SEQ ID NO 27; 107pp; English.
 X X
 X X The invention relates to novel isolated human secreted polypeptides (I)
 X X and polynucleotides (II) such as arthritis, nephritis, Crohn's disease,
 X X inflammation, reperfusion injury, shock, sepsis, immune responses, and is
 X X involved in increasing haemophagocytosis, stem cell survival, bone growth
 X X and remodeling. (I), (II) and modulators of (II) are useful for
 X X prophylaxis or treatment of one or more cancers. (II) is also useful for
 X X creating transgenic animals useful for studying the in vivo activities of
 X X the polypeptide as well as for studying molecular mechanisms of nerve
 X X (I) induces the proliferation of the treatment of central and
 X X peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 X X Parkinson's disease, Huntington's disease, and amyotrophic lateral
 X X sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 X X activity, regulation of haematopoiesis and is useful for treating myeloid
 X X or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 X X and for regeneration of bone, cartilage, tendon, ligament, salivary
 X X tissue growth, and in tissue repair. Neutrophils home degenerative
 X X ulcers, for treating Crohn's disease, psoriasis, rheumatoid arthritis,
 X X distal arteriole occlusion disease. Furthermore, (I) is also useful for
 X X distal arteriole occlusion disease, reperfusion injury in lung or liver fibrosis,
 X X reperfusion injury in various tissues, various immune deficiencies and
 X X disorders including severe combined immunodeficiency (SCID), bacterial or
 X X fungal infections, autoimmune disorders e.g. multiple sclerosis,
 X X rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic

[illegible]



GenCore version 4.5
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OK nucleic - nucleic search, using sw model

Run on: June 23, 2002, 15:09:02 : Search time 167.81 seconds
(without alignments)

Title: US-09-747-514a-3
.. 35,110 Million cell updates/sec

Perfect score: 24

Sequence: 1 ccgttgagcgagcgagcgagcccg 24

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/pdata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C	2	11.4	72.5	1459	3	US-08-303-861-17	Sequence 17, Appl
C	3	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
C	4	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
C	5	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
C	6	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
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C	12	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
C	13	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
C	14	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
C	15	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
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C	21	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
C	22	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
C	23	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
C	24	16.2	67.5	1390	2	US-08-421-443-10	Sequence 19, Appl
C	25	15.8	65.8	8056	3	US-08-934-131-2	Sequence 14, Appl
C	26	15.8	65.8	8056	3	US-08-934-131-2	Sequence 14, Appl
C	27	15.8	65.8	8056	3	US-08-934-131-2	Sequence 14, Appl

C	28	15.8	65.8	8052	1	US-08-103-785-1	Sequence 1, Appl
C	29	15.8	65.8	8052	1	US-08-103-785-1	Sequence 28, Appl
C	30	15.8	65.8	4403765	4	US-09-103-840A-28	Sequence 2, Appl
C	31	15.8	65.8	4403765	4	US-09-103-840A-28	Sequence 2, Appl
C	32	15.8	65.8	4411529	4	US-09-103-840A-1	Sequence 286, Appl
C	33	15.6	65.0	50341	2	US-08-060-756-286	Sequence 1, Appl
C	34	15.6	65.0	50341	2	US-08-060-756-286	Sequence 1, Appl
C	35	15.6	65.0	50341	2	US-08-060-756-286	Sequence 1, Appl
C	36	15.6	65.0	50341	2	US-08-060-756-286	Sequence 1, Appl
C	37	15.4	64.2	11752	3	US-08-425-436-1	Sequence 12, Appl
C	38	15.4	64.2	11752	3	US-08-425-436-1	Sequence 12, Appl
C	39	15.4	64.2	2990	1	US-08-572-951-1	Sequence 1, Appl
C	40	15.4	64.2	2990	1	US-08-572-951-1	Sequence 1, Appl
C	41	15.4	64.2	3186	2	US-08-761-258-8	Sequence 8, Appl
C	42	15.2	63.3	35	3	US-08-159-274-34	Sequence 34, Appl
C	43	15.2	63.3	35	3	US-08-159-274-34	Sequence 36, Appl
C	44	15.2	63.3	35	3	US-08-159-274-34	Sequence 36, Appl
C	45	15.2	63.3	57	4	US-09-401-697-25	Sequence 29, Appl

ALIGNMENTS

RESULT

US-08-303-861-17/c
Sequence 17, Application US/08303861

Patent No. 6086902

GENERAL INFORMATION:

APPLICANT: ZAMB, TIMOTHY

INVENTOR: ZAMB, TIMOTHY

APPLICANT: ZAMB, TIMOTHY

TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: MORRISON & FORSTER

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/303,861

FILING DATE: 09-SEP-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: K 35 636

REFERENCE/DOCKET INFORMATION: 29310-20020.20

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 1499 base pairs

TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

FEATURE KEY: CDS

LOCATION: 390..1163

US-08-303-861-17

Query Match: 72.5% Score 17.4; DB 3; Length 1499;
Identical Similarity 94.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TELEFAX: (510) 559-3111

LOCATION: 1..390


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1      LOCATION: 1..6170 /note= "SEQ ID NO:4 contains genes
2      OTHER INFORMATION: involved in synthesis, and modulation of synthesis
3      OTHER INFORMATION: of PHL."
4      US-08-434-507-4
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6      Query Match
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8      Best Local Similarity 67.5%; Score 16.2; DB 2; Length 6170;
9      Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0
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11     ||||| ||||| |||||
12     Db 5915 cccctccggcgccggagagacc 5935
13
14 RESULT 8
15 PCT-US96-10986-4
16 Sequence 4, Application PC/7059610986
17 GENETIC INFORMATION:
18 TITLE OF INVENTION: Sequences for Production of
19 TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods
20 NUMBER OF SEQUENCES: 20
21 CORRESPONDENCE ADDRESS:
22 ADDRESSEE: Stephan A. Pendorf, DOMINK & STEIN
23 STREET: 600 N. West Shore Boulevard, Suite 1000
24 CITY: Tampa
25 STATE: FL
26 COUNTRY: USA
27 ZIP: 33609
28 COMPUTER READABLE FORM:
29 MEDIUM TYPE: Floppy disk
30 COMPUTER: IBM PC compatible
31 OPERATING SYSTEM: Windows NT
32 SOFTWARE: Protein Release #1.0, Version #1.25
33 CURRENT APPLICATION DATA:
34 APPLICATION NUMBER: PCT/US96/10986
35 FILING DATE:
36 CLASSIFICATION:
37 ATTORNEY/AGENT INFORMATION:
38 NAME: Pendorf, Stephan A.
39 REFERENCE NUMBER: 32665
40 TELECOMMUNICATION INFORMATION:
41 TELEPHONE: (813) 289-2966
42 TELEFAX: (813) 289-2967
43 INFORMATION FOR SEQ ID NO: 4:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 6170 base pairs
46 TYPE: nucleic acid
47 STRANDNESS: single
48 TOPOLOGY: linear
49 MOLECULE TYPE: DNA (genomic)
50 HYPOTHETICAL: NO
51 ANTI-SENSE: NO
52 ORIGINAL SOURCE:
53 ORGANISM: Pseudomonas fluorescens
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 LOCATION: 5781..6170
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 OTHER INFORMATION: involved in synthesis, and modulation of synthesis
 OTHER INFORMATION: of Ph.I."
 PCT-US96-10986-4

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 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 Db 5915 cccctcggggcgagagagacc 5935

RESULT 9
 US-08-494-907-3
 Sequence 3 Application US/08494907
 INVENTION: 55238
 GENERAL INFORMATION:
 APPLICANT: Thomasow, Linda S
 APPLICANT: Bangera, Malaxmi
 APPLICANT: Weller, David M
 APPLICANT: Cook, R. James
 TITLE OF INVENTION: Sequences for Production of
 NUMBER OF SEQUENCES: 2
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Margaret A. Connor, USDA-ARS
 STREET: 800 Buchanan Street
 CITY: Albany
 STATE: CA
 COUNTRY: USA
 ZID: 94410
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 PILING DATE
 PILING NUMBER: US/08/494, 907
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Connor, Margaret A
 REGISTRATION NUMBER: 30043
 REFERENCE/DOCKET NUMBER: 0009, 95
 TELEPHONE: (510) 559-5777
 TELEFAX: (510) 559-5777
 INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 6387 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 RECOMBINATION: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas fluorescens
 FEATURE:
 NAME/KEY: misc-feature
 LOCATION: complement (4285..5076)
 OTHER INFORMATION: /note="Ph.D, transcribed from
 OTHER INFORMATION: right to left"
 FEATURE: right to left"
 NAME/KEY: misc-feature
 LOCATION: complement (2606..3313)
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 OTHER INFORMATION: /note="Ph.D, transcribed from left
 OTHER INFORMATION: to right"
 FEATURE: transcribed from left
 NAME/KEY: misc-feature
 LOCATION: 1..6387
 OTHER INFORMATION: /note="SDO ID NO:3 contains genes
 OTHER INFORMATION: involved in synthesis and modulation of synthesis
 OTHER INFORMATION: of Ph.I."
 US-08-494-907-3

Query Match 67.5%; Score 16.2; DB 2; Length 6387;
 Best Local Similarity 85.7%; Pred. NO. 1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 cccctcggggcgagagagacc 21
 Db 5915 cccctcggggcgagagagacc 5935

RESULT 10
 PCT-US96-10986-3
 Sequence 3 Application PC/TUS9610986
 INVENTION: 55238
 GENERAL INFORMATION:
 TITLE OF INVENTION: Sequences for Production of
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Stephan A. Rendorf, DOMINIK & STEIN
 STREET: 600 N. West Shore Boulevard, Suite 1000

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RESULT  11
US-08-188-281B-8
? Sequence 8, Application US/08188281B
? Patent No. 5610093
? GENERAL INFORMATION:
? APPLICANT: MATANABE, SHINICHI
? APPLICANT: YAMAGUCHI, JUDIE
? APPLICANT: SHIMIZU, SHINJI
? APPLICANT: DEJARE, SUZUKI, G.
? TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
? TITLE OF INVENTION: ENVELOPE GENES
? NUMBER OF SEQUENCES: 22
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: ABBOTT LABORATORIES D377/A6D
? STREET: ONE ABBOTT PARK ROAD
? CITY: ABBOTT PARK
? STATE: ILL
? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? FILING DATE: 05/08/1980, 281B
? PRIORITY NUMBER:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: FOREMSKI, PRISCILLA E.
? REGISTRATION NUMBER: 33,207
? REFERENCE/DOCKET NUMBER: 5521, US-01
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 708/3936365
? TELEFAX: 708/3839635
? INFORMATION FOR SEQ ID NO: 8:
? LENGTH: 7106 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? FEATURE: CDS
? LOCATION: 922..2022
US-08-188-281B-8

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Best Local Similarity 85.7%; Pred. No. 1e-02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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? Sequence 5, Application US/08453552
? Patent No. 5667392
? GENERAL INFORMATION:

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1 APPLICANT: CASEY, JAMES M.
2 APPLICANT: BODE, SUZANNE L.
3 APPLICANT: ZECK, BILLY J.
4 APPLICANT: YAMAGUCHI, JULIE
5 APPLICANT: FRAIL, DONALD E.
6 APPLICANT: DESAI, SURESH M.
7 APPLICANT: DEVARE, SUSHIL G.
8 TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
9 NUMBER OF SEQUENCES: 12
10 CORRESPONDENCE ADDRESS:
11 ADDRESSES: ABBOTT LABORATORIES D377/AP6D
12 CITY: ONE ABBOTT PARK ROAD
13 STATE: IL
14 COUNTRY: USA
15 ZIP: 60064-3500
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patentin Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/453,552
23 FILING DATE:
24 CLASSIFICATION: 435
25 ATTORNEY/AGENT INFORMATION:
26 NAME: FOREMSKI, PRISCILLA E.
27 REGISTRATION NUMBER: 33,207
28 REFERENCE/DOCKET NUMBER: 5131.US.D1
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 708-937-6365
31 TELEFAX: 708-937-9556
32 INFORMATION FOR SEQ ID NO: 5:
33 SEQUENCE CHARACTERISTICS:
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: circular
37 MOLECULE TYPE: DNA (genomic)
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: 922..2022
41 US-08-453-552.5
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43 Query Match 67.5%; Score 16.2; DB 1; Length 7106;
44 Best Local Similarity 85.7%; Pred. No. 1e+02;
45 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
46
47 Oy 4 ttccggcgcgaggaagcccg 24
48 Db 912 ttccggcgcgatctgcgccg 932
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50 RESULT 13
51 US-08-710-637-5
52 Sequence 5, Application US/08710637
53 GENERAL INFORMATION:
54 APPLICANT: CASEY, JAMES M.
55 APPLICANT: BODE, SUZANNE L.
56 APPLICANT: ZECK, BILLY J.
57 APPLICANT: YAMAGUCHI, JULIE
58 APPLICANT: FRAIL, DONALD E.
59 APPLICANT: DESAI, SURESH M.
60 APPLICANT: DEVARE, SUSHIL G.
61 TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
62 NUMBER OF SEQUENCES: 12
63 CORRESPONDENCE ADDRESS:
64 ADDRESSES: ABBOTT LABORATORIES D377/AP6D
65 STREET: ONE ABBOTT PARK ROAD

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1 CITY: ABBOTT PARK
2 STATE: IL
3 COUNTRY: USA
4 ZIP: 60064-3500
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patentin Release #1.0, Version #1.25
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/710,637
12 FILING DATE:
13 CLASSIFICATION: 435
14 PRIOR APPLICATION DATA:
15 PCT APPLICATION NUMBER: US/08/144,099
16 FILING DATE:
17 APPLICATION NUMBER: US 07/830,024
18 FILING DATE: 01-JAN-1992
19 ATTORNEY/AGENT INFORMATION:
20 NAME: FOREMSKI, PRISCILLA E.
21 REGISTRATION NUMBER: 33,207
22 REFERENCE/DOCKET NUMBER: 5131.US.01
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 708-937-6365
25 TELEFAX: 708-937-9556
26 INFORMATION FOR SEQ ID NO: 5:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 7106 base pairs
29 TYPE: nucleic acid
30 STRANDEDNESS: single
31 TOPOLOGY: circular
32 MOLECULE TYPE: DNA (genomic)
33 FEATURE:
34 NAME/KEY: CDS
35 LOCATION: 922..2022
36 US-08-710-637-5
37
38 Query Match 67.5%; Score 16.2; DB 2; Length 7106;
39 Best Local Similarity 85.7%; Pred. No. 1e+02;
40 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
41
42 Oy 4 ttccggcgcgaggaagcccg 24
43 Db 912 ttccggcgcgatctgcgccg 932
44
45 RESULT 14
46 PCT-US93-00907-5
47 Sequence 5, Application PC/TUS9300907
48 GENERAL INFORMATION:
49 APPLICANT: CASEY, JAMES M.
50 APPLICANT: BODE, SUZANNE L.
51 APPLICANT: ZECK, BILLY J.
52 APPLICANT: YAMAGUCHI, JULIE
53 APPLICANT: FRAIL, DONALD E.
54 APPLICANT: DESAI, SURESH M.
55 APPLICANT: DEVARE, SUSHIL G.
56 TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
57 NUMBER OF SEQUENCES: 12
58 CORRESPONDENCE ADDRESS:
59 ADDRESSES: ABBOTT LABORATORIES D377/AP6D
60 STREET: ONE ABBOTT PARK ROAD
61 CITY: ABBOTT PARK
62 STATE: IL
63 COUNTRY: USA
64 ZIP: 60064-3500
65 COMPUTER READABLE FORM:
66 MEDIUM TYPE: Floppy disk
67 OPERATING SYSTEM: PC-DOS/MS-DOS
68 SOFTWARE: Patentin Release #1.0, Version #1.25

```

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/00907
 FILING DATE: 19930129
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: FORDEBSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6265
 TELEFAX: 708-937-6265
 INVENTOR:
 NAME: SURESH N.
 LENGTH: 7106 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 922..2022
 PCT-US93-00907-5

Query Match 67.5%; Score 16.2; DB 5; Length 7106;
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 Matches 18; Conservative 0; Mismatches 3;

OY 4 ttcggggcgaggaagcccg 24
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 DB 912 TTGGGGCGGATCTGCCCG 932

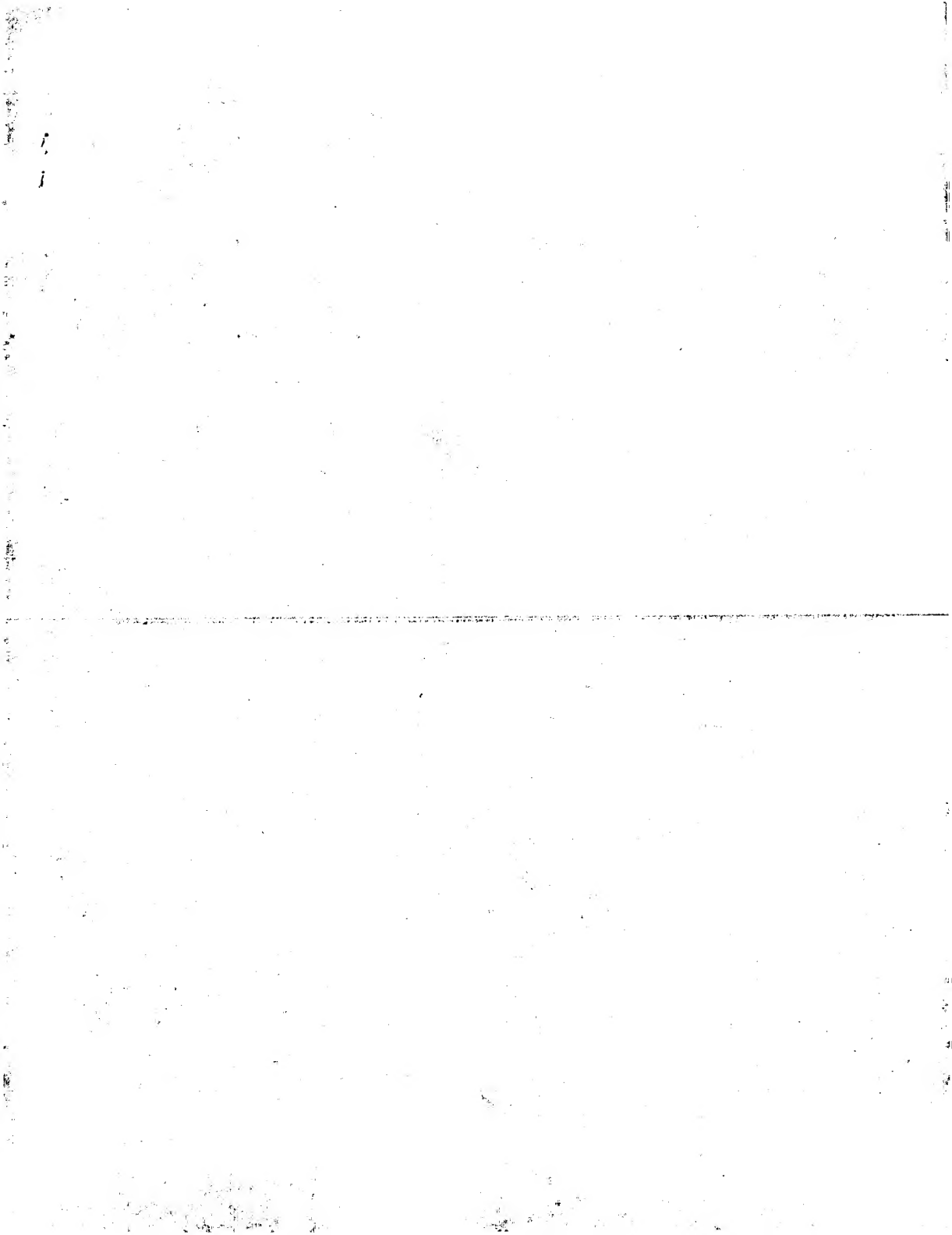
RESULT 15

PCT-US94-07280-8
 Sequence 8, Application PC/TUS9407280
 GENERAL INFORMATION:
 APPLICANT: MATINABE, SHINICHI
 APPLICANT: YAMAGUCHI, JULIE
 APPLICANT: DESAI, SURESH N.
 APPLICANT: SURESH N.
 TITLE OF INVENTION: HUMANILAN EXPRESSION SYSTEMS FOR HCV
 TITLE OF INVENTION: ENVELOPE GENES
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP60
 STREET: ONE ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PREDICI, Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/07280
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: FORDEBSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6265
 TELEFAX: 708-937-6265
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7106 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 922..2022
 PCT-US94-07280-8

Query Match 67.5%; Score 16.2; DB 5; Length 7106;
 Best Local Similarity 85.7%; Pred. No. 1e+02; 3; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 3;
 OY 4 ttcggggcgaggaagcccg 24
 ||||||||| | |||||
 DB 912 TTGGGGCGGATCTGCCCG 932

Search completed: June 23, 2002, 15:09:16
 Job time: 78580 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW nucleic - nucleic search, using SW model

Run on: June 23, 2002, 06:32:15 / Search time 2161.72 Seconds

(Without alignments)
212,971 Million cell updates/sec

Title: US-09-747-514a-4

Perfect score: 1 gaagcgccgtagcgccggcggtc 22

Sequence: IDENTITY_NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 1046328293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing files 45 summaries

Database : GenBank:
1: gb.ba:*
2: gb.hcg:*
3: gb.in:*
4: gb.lm:*
5: gb.lm:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.ro:*
12: gb.ro:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.in:*
20: em.in:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.ro:*
28: em.un:*
29: em.vi:*
30: em.hcg.hum:*
31: em.hcg.in:*
32: em.hcg.other:*
33: em.hcg.in:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

Result	Query	Match	Length	DB	ID	Description
1	22	100.0	3123	1	PU8241	038241 Pseudomonas
2	22	100.0	13075	1	AC094113	AC094113 Pseudomonas
3	17.8	80.9	91686	2	AC094113	AC094113 Pseudomonas
4	17.4	79.1	10968	1	AE002062	AE002062 Pseudomonas
5	17.4	79.1	44273	1	AY028171	AY028171 Pseudomonas
6	17.2	78.2	2317	1	HSU05365	HSU05365 Pseudomonas
7	17.2	78.2	4287	1	HSU05365	HSU05365 Pseudomonas
8	17.2	78.2	4287	1	HSU05365	HSU05365 Pseudomonas
9	17.2	78.2	4287	1	HSU05365	HSU05365 Pseudomonas
10	17.2	78.2	28965	2	AC094168	AC094168 Pseudomonas
11	17.2	78.2	38793	1	MSGB27CS	MSGB27CS Pseudomonas
12	17.2	78.2	65469	2	AC015511	AC015511 Pseudomonas
13	17.2	78.2	100814	2	AC017402	AC017402 Pseudomonas
14	17.2	78.2	104228	3	AC005269	AC005269 Pseudomonas
15	17.2	78.2	104228	3	AC005269	AC005269 Pseudomonas
16	17.2	78.2	120111	2	AC010000	AC010000 Pseudomonas
17	17.2	78.2	120111	2	AC010000	AC010000 Pseudomonas
18	17.2	78.2	121788	2	AC023470	AC023470 Pseudomonas
19	17.2	78.2	126682	9	AC008649	AC008649 Pseudomonas
20	17.2	78.2	135259	9	AC004590	AC004590 Pseudomonas
21	17.2	78.2	179504	2	AC0073149	AC0073149 Pseudomonas
22	17.2	78.2	179527	2	AC0073149	AC0073149 Pseudomonas
23	17.2	78.2	191726	3	AC008602	AC008602 Pseudomonas
24	17.2	78.2	191726	3	AC008602	AC008602 Pseudomonas
25	17.2	78.2	197244	2	AC008649	AC008649 Pseudomonas
26	17.2	78.2	205516	9	AC008781	AC008781 Pseudomonas
27	17.2	78.2	273785	1	SMES91793	SMES91793 Pseudomonas
28	17.2	78.2	302473	3	AE003589	AE003589 Pseudomonas
29	17.2	78.2	348450	1	MLBPRV4	MLBPRV4 Pseudomonas
30	17.2	78.2	348450	1	MLBPRV4	MLBPRV4 Pseudomonas
31	16.8	76.4	105113	2	AC010465	AC010465 Pseudomonas
32	16.8	76.4	123062	2	AC098359	AC098359 Pseudomonas
33	16.8	76.4	123062	2	AC098359	AC098359 Pseudomonas
34	16.8	76.4	159587	2	AP003528	AP003528 Pseudomonas
35	16.8	76.4	161798	2	AP003528	AP003528 Pseudomonas
36	16.8	76.4	165202	2	AP003491	AP003491 Pseudomonas
37	16.8	76.4	172221	2	AC0106194	AC0106194 Pseudomonas
38	16.4	74.5	105211	2	AC007873	AC007873 Pseudomonas
39	16.4	74.5	105211	2	AC007873	AC007873 Pseudomonas
40	16.4	74.5	30000	6	AX250261	AX250261 Pseudomonas
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42	16.4	74.5	164839	2	AC105823	AC105823 Pseudomonas
43	16.2	73.6	635	9	HSN342413	HSN342413 Pseudomonas
44	16.2	73.6	820	33	AC076948	AC076948 Pseudomonas
45	16.2	73.6	1454	9	HSN801746	HSN801746 Pseudomonas
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ALIGNMENTS

RESULT 1
LOCUS PU8241
DEFINITION Pseudomonas aeruginosa ornithine decarboxylase (orc) and Pseudomonas
catalbolic repression control protein (orc) and Pseudomonas
genes, complete cds.
ACCESSION U08241.1 GI:1079660
VERSION 1.0
KEYWORDS Pseudomonas aeruginosa strain PAOI.
SOURCE Pseudomonas aeruginosa
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE 1 (bases 1 to 3123)
AUTHORS MacGregor,C.H., Atore,S.K., Hager,P.W., Dall,M.B. and Philbs,P.V.
TITLE The nucleotide sequence of the Pseudomonas aeruginosa pyrC-crc-rph
region and the purification of the pyrC gene product
JOURNAL J. Bacteriol. 178 (10): 5627-5635 (1996)
MEDLINE 96421989
REFERENCE 2 (bases 1 to 3123)
AUTHORS Hager,P.W. and Philbs,P.V. Jr.
TITLE Direct Submission

REFERENCE
AUTHORS

Mammalia: Eutheria; Rodentia: Sciurognathi; Muridae; Murinae;

1 (bases 1 to 91686)

Murphy, D.M., Adams, C., Adlo-Oduola, B., Altman, F.R., Allen, C.,

Alston, J., Alston, J., Alston, J., Alston, J., Alston, J., Alston, J.,

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As not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 6013: contig of 6013 bp in length

6014 6013: gap of unknown length

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6016 6013: gap of unknown length

6017 6013: gap of unknown length

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6053 6013: gap of unknown length

6054 6013: gap of unknown length

* Identifying clones that may be gene-rich and allows
 * overlapping relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the accessions updated, the accession number will
 * be preserved.

1 915: contig of 915 bp in length
 916 1015: gap of 100 bp
 1016 1923: contig of 908 bp in length
 1924 2023: gap of 100 bp
 2024 2898: contig of 875 bp in length
 2899 3157: gap of 100 bp in length
 3160 4017: gap of 100 bp in length
 4018 4951: contig of 934 bp in length
 4952 5051: gap of 100 bp in length
 5052 5959: contig of 908 bp in length
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 8131 9064: contig of 934 bp in length
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FEATURES
 SOURCE
 1) Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="RP11-21011"
 /clone_id="RP11-21011"

BASE COUNT 12967 a 14096 c 13532 g 16748 t 6846 others
 ORIGIN

Query Match 78.2% Score 17.2: DN2: Length 64189;
 Best Local Similarity 86.4% Pred. 1.4e+03;
 Matches 19: Conservative 0: Mismatches 3: Indels 0: Gaps 0:
 GY 1 gaagcgccatagccgggagc 22

Db 22327 GAAGCGCGCCAGCCCGCGGTC 22306

RESULT 13
AC017402/c 65467 bp DNA linear HTG 09-DEC-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.

ACCESSION AC017402
VERSION AC017402.1 GI:6553584
KEYWORDS HTG; HTGS; PHASE2.
SOURCE Fruit fly, melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyroidae; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 65467)
AUTHORS Adams, M. and Venter, J.C.
TITLES Direct Submission
JOURNAL Submitted (29-DEC-1999) Colaba Genomics, 45 West Gude Drive, Gaithersburg, MD, USA
COMMENT This sequence was identified as CD1:0210598 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession/Qualifiers
1. 65467

FEATURES
source
/db_xref="taxon:7277"
BASE COUNT 18712 a 14536 c 14336 g 17873 t

ORIGIN

Query Match 78.2% Score 17.2; DB 2; Length 65467;
Best Local Similarity 86.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0

Db 10339 GAGCGCGCTAGCGCGGATC 22

RESULT 14
AP003929 100814 bp DNA linear HTG 19-JUN-2001
LOCUS Oryza sativa chromosome 10
DEFINITION Oryza sativa chromosome 10
ACCESSION AP003929
VERSION AP003929.1 GI:14915712
KEYWORDS HTG; HTGS; PHASE2.
SOURCE Oryza sativa (cultivar: Nipponbare) DNA, clone: OJ1240.G08.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Oryzaceae; Oryza.
AUTHORS Sasaki, T., Matsumoto, T., and Yamamoto, K.
TITLES Oryza sativa nlpdbare(NA3) genomic DNA, chromosome 7, BAC
clone: OJ1240.G08
JOURNAL Published only in database (2001) In press
2 (bases 1 to 100814)
DIRECT SUBMISSION
SUBMITTED (18-JUN-2001) Tsukui Sasaki, National Institute of
Agricultural Resources, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://irgp.dna.affrc.go.jp/
Tel: 81-298-38-7441, Fax: 81-298-38-7441)
COMMENT The nucleotide sequence of this BAC clone was generated by
combining HindIII and Rsp-III Japan sequencing data.

Db 97427 GAAGCGCGCTCGCGCGCGGTC 97448

RESULT 15
AC005269 104278 bp DNA linear HTG 07-JUN-1998
LOCUS Drosophila melanogaster DNA sequence (Pis DS00764 (D273) and
DEFINITION Drosophila melanogaster DNA sequence (Pis DS00764 (D273) and
ACCESSION AC005269
VERSION AC005269.1 GI:3293208
KEYWORDS HTG
SOURCE Drosophila melanogaster (Subclones in tet from P1 clones DS00764 (D273) and DS00501 (D274) DNA.
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyroidae; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 104278)
AUTHORS Gelink, S.E., George, R.A., Galle, R.F., Hoskins, R.A., Baxter, E., Blazer, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummel, S.R., Madza, P., Mok, M.S., Kim, S.H., Lee, B., Lomoran, M.A., Mak, J., Maza, P., Mok, M.S., Mosher, A.R., Mosher, A.R., Nixon, K., Pacheco, J.M., Park, S., Pfeiffer, B., Puneh, E., Sait, E., Twomey, B., Wan, K.H., White, K.R., Yee, A., Zhang, R., Zieren, L.L., and Kimmel, B.
TITLES Sequencing of Drosophila chromosome, region 21C3-21C7
JOURNAL Unpublished (1997)
2 (bases 1 to 104278)
AUTHORS Gelink, S.E., George, R.A., Galle, R.F., Hoskins, R.A., Baxter, E., Blazer, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummel, S.R., Madza, P., Mok, M.S., Kim, S.H., Lee, B., Lomoran, M.A., Mak, J., Maza, P., Mok, M.S., Mosher, A.R., Mosher, A.R., Nixon, K., Pacheco, J.M., Park, S., Pfeiffer, B., Puneh, E., Sait, E., Twomey, B., Wan, K.H., White, K.R., Yee, A., Zhang, R., Zieren, L.L., and Kimmel, B.
TITLES Direct Submission
JOURNAL Submitted (1998) Berkeley Drosophila Genome Project, MS
Berkeley, CA 94720, US
COMMENT Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720

and relationship to other sequences, please visit our sequence archive web site (<http://fruitfly.berkeley.edu/sequence/>) or send email to drosophilaemmc@lbl.gov.

FEATURES

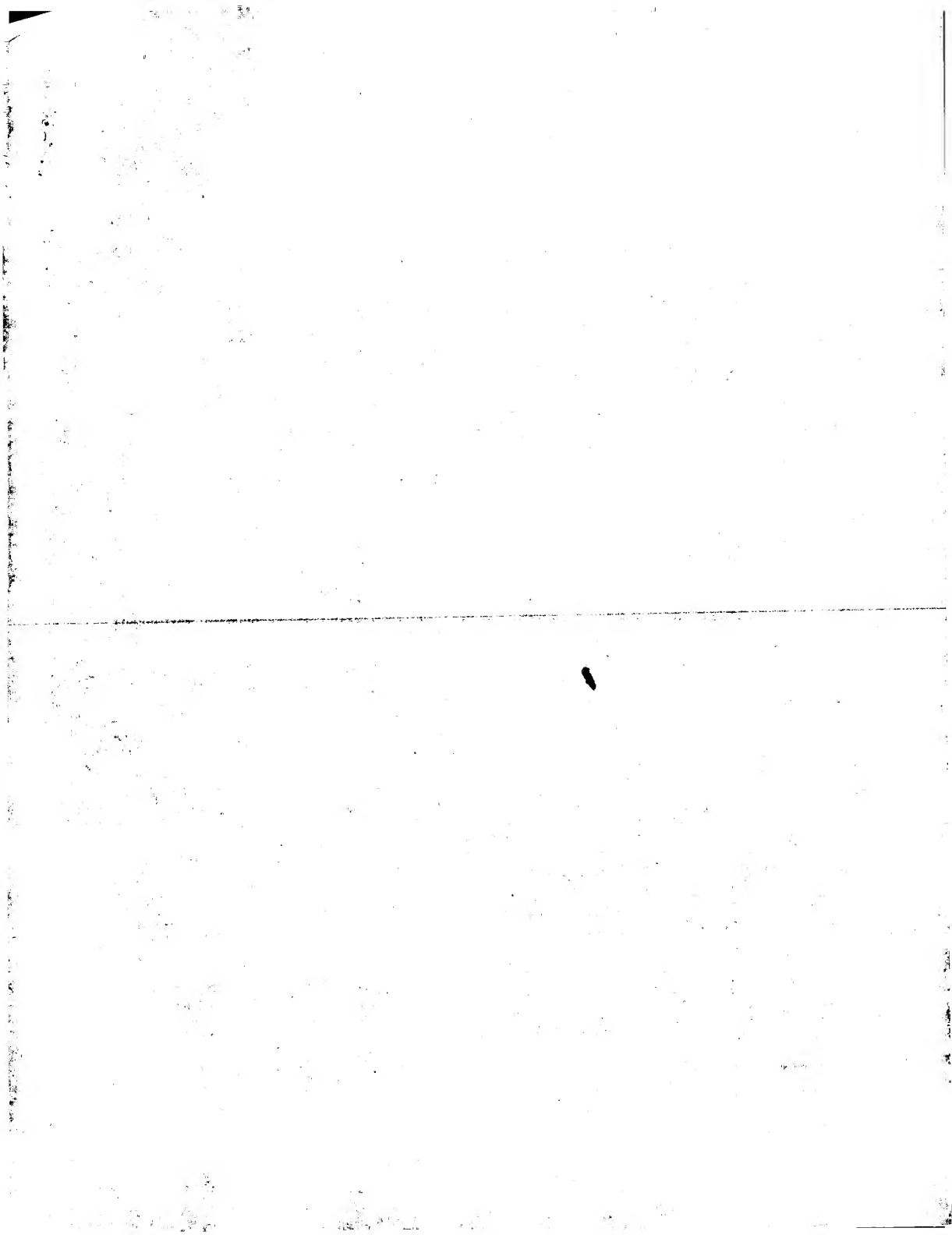
Library locations: 135-8, 21-6.
 Location: 104278
 1 104278
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 /db_xref="taxon:7227"
 /chromosome="2L"
 /map="21C3-21C7"
 /clone="P18 DS00764 (D273) and DS00501 (D274)"
 /note="DS00764 (D273) extends from bp 1 to bp 38,674 and DS00501 (D274) extends from bp 20,505 to bp 104,278."*

BASE COUNT 28186 a 23704 c 23278 g 23110 t

ORIGIN

Query Match 78.2%; Score 17.2; DB 3; Length 104278;
 Percent Identical Similarity 86.4%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 gaagcgagctagcgccgaggtc 22
 |||||
 Db 78982 GAAGCGGCGTGGCCGCGGCGC 79003

Search completed: June 23, 2002, 06:32:29
 Job time: 63881 sec



PI Isaia J;
 XX WPI: 2001-244777/25.
 DR New nucleic acid molecule for use as a marker for screening cancer,
 XX comprises the coding region for a T-type calcium channel and regulatory
 PT sequences associated with the channel -
 XX
 XX Claim 32: Fig 4A: 125bp. English.
 XX
 XX The present sequence for human T-type calcium channel CACNA1C Cpg island
 CC 1 and 2 is located within the CACNA1C gene. CACNA1C encodes a T-type
 CC chromosome 17. The methylation state of specific regions within Cpg
 CC islands associated with the CACNA1C gene correlate with several cancers
 CC phenotypes involving various tissue and cell types. Since aberrant in
 CC methylation of normally unmethylated Cpg islands is often observed in
 CC immunolabelled and transformed cells, CACNA1C is implicated in cellular
 CC proliferative disorder e.g. leukemia, colorectal, lung, breast and
 CC other cancers. This sequence is a T-type calcium channel Cpg island
 CC containing primers (AS01574-AS01673) for amplification of a
 CC Cpg-containing nucleic acid, where the primer hybridizes with a target
 CC polynucleotide sequence (AS01677-AS01676), can be used for detecting
 CC selected methylation. The Cpg island sequences (AS01677-AS01692) are
 CC selected from genes encoding CACNA1C, apolipoprotein B (APOB), caudal
 CC type homeobox 3, transcription factor 2, CDX2), epithelial growth factor
 CC (EGF), heat shock 70KD protein 6 (HSP70), HSP96), RasGAP-related
 CC (GRP78), Klotho (KL), proteinase-activated receptor 2 (PAR2),
 CC protein (IGFBP2), Klotho (KL), proteinase-activated receptor 2 (PAR2),
 CC paired-like homeodomain transcription factor 2 (PTX2), patched A and B
 CC (PTCH); PTCHB) and syndecan 1 and 4 (SDC1; SDC4) or a MINT31 sequence.
 XX
 XX Sequence 2093 BP: 295 A; 695 C; 913 G; 300 T; 0 other:
 SQ
 Query Match 78.2%; Score 17.2; DB 22; Length 2093;
 Best Local Similarity 86.4%; Pred. No. 2, 1e-02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 gaagcgagcgtagccggggagtc 22
 DB 728 GCAAGCGCGAGAGCCGCGGCGTC 707
 RESULT 2
 AAL36954
 ID AAL36954 standard; DNA; 5846 BP.
 XX
 XX AAL36954:
 DT 08-JAN-2002 (first entry)
 XX
 XX Human musculoskeletal system related polynucleotide SEQ ID NO 3319.
 DE
 XX Cytostatic; immunosuppressive; nocotropic; neuroprotective; antiviral;
 KM antitumor; hepatocytic; antileukemic; antiproliferative; antitumor;
 KM cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KM neurological disease; infection; human; secreted protein;
 KM musculoskeletal system; ds.
 XX
 XX Homo sapiens.
 OS
 XX W0200155367-A1.
 XX
 XX 02-AUG-2001.
 PD
 XX
 XX 17-JAN-2001; 2001MO-US01338.
 PF
 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180528.
 PR 25-FEB-2000; 2000US-0184554.
 PR 02-MAR-2000; 2000US-0189350.

PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190766.
 PR 18-APR-2000; 2000US-0200579.
 PR 18-MAR-2000; 2000US-0205512.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216447.
 PR 07-JUL-2000; 2000US-0216980.
 PR 11-JUL-2000; 2000US-0217482.
 PR 11-JUL-2000; 2000US-0218990.
 PR 26-JUL-2000; 2000US-0218990.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
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 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225266.
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 PR 14-AUG-2000; 2000US-0225270.
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 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
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 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226688.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228287.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229344.
 PR 05-SEP-2000; 2000US-0229345.
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 PR 05-SEP-2000; 2000US-0230437.
 PR 05-SEP-2000; 2000US-0230437.
 PR 05-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232080.
 PR 14-SEP-2000; 2000US-0232397.
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 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233063.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 25-SEP-2000; 2000US-0234998.
 PR 25-SEP-2000; 2000US-0235844.
 PR 27-SEP-2000; 2000US-0235844.
 PR 27-SEP-2000; 2000US-0235844.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.

PR 13-OCT-2000; 2000US-0239935.
 PR 20-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241721.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241826.
 PR 20-OCT-2000; 2000US-0241828.
 PR 01-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246533.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250191.
 PR 05-DEC-2000; 2000US-0251980.
 PR 05-DEC-2000; 2000US-0251981.
 PR 05-DEC-2000; 2000US-0251986.
 PR 05-DEC-2000; 2000US-0251987.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0251989.
 PR 05-DEC-2000; 2000US-0251990.
 PR 05-DEC-2000; 2000US-0251997.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-451937/48.
 Isolated polypeptide for treating, preventing and/or prognosing
 disorders related to the musculoskeletal system including
 musculoskeletal cancers and also for testing and detection e.g.
 diagnosis -
 Example 2: SEQ ID NO 3319; 781bp + Sequence Listing; English.

CC The invention relates to novel genes (AAL36955-AAL37666) and proteins
 CC (AAB03087-AB04100) associated with the musculoskeletal system useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment
 CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
 CC (b) infectious diseases such as viral, bacterial, fungal and
 CC gastrointestinal tract, liver, gland, bone, bone marrow, breast,
 CC disorders e.g. Addison's disease, allergies, autoimmune hemolytic
 CC anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic diseases.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WFO at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence 5846 BP; 1109 A; 1894 C; 1739 G; 1104 T; 0 other;
 Query Match 78.2%; Score 17.7; DB 22; Length 5846;
 Best Local Similarity 86.4%; Pred. No. 1.9e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 gaagcgctaggcgccgggagtc 22
 Db 971 gaagcgcgagcgagcgagcgagtc 992
 RESULT 3
 AAL36955
 ID AAL36955 standard; DNA: 5848 BP.
 XX
 XX AAL36955;
 PD 08-JAN-2002 (first entry)
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 3320.
 DE
 XX
 XX Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;
 XX antiherpetic; hepatotropic; antidiabetic; antihistaminic; antitumor;
 XX antiangiogenic; antiparasitic; antiparasitic; antiparasitic;
 XX cardiotonic; gene therapy; cancer; antiparasitic; antiparasitic;
 XX neurological disease; infection; human, secreted protein;
 XX musculoskeletal system; ds.
 XX
 OS Homo sapiens.
 XX
 XX MO200155367-A1.
 PD 02-AUG-2001.
 XX
 PD 17-JAN-2001; 2001WO-US01338.
 XX
 XX 31-JAN-2000; 2000US-0179065.
 XX 31-JAN-2000; 2000US-0180628.
 XX 24-FEB-2000; 2000US-0186350.
 XX 02-MAR-2000; 2000US-0186350.
 XX 16-MAR-2000; 2000US-0189874.
 XX 17-MAR-2000; 2000US-0190076.
 XX 18-APR-2000; 2000US-0198123.
 XX 19-MAY-2000; 2000US-0205515.
 XX 20-MAY-2000; 2000US-0205515.
 XX 26-JUN-2000; 2000US-0204662.
 XX 30-JUN-2000; 2000US-0215135.
 XX 07-JUL-2000; 2000US-0215647.
 XX 07-JUL-2000; 2000US-0215880.
 XX 11-JUL-2000; 2000US-0217487.
 XX 11-JUL-2000; 2000US-0217486.
 XX 14-JUL-2000; 2000US-0218290.

[illegible]

CC sequence encodes a novel secreted protein of the invention.
 Query Match 73.6%; Score 16.2; DB 22; Length 664;
 Best Local Similarity 85.7%; Pred. No. 6e+02; 3; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 0Y 2 aagcgctgtagccgggggctc 22
 |||||||
 Db 49 AGCGCGTGAAGCCAGCCGCTC 29

RESULT 7
 ID AAK92231 standard; cDNA: 780 BP.
 AC AAK92231;
 AC AAK92231;
 AC 06-NOV-2001 (first entry)
 DE Human cDNA 5'-end sequence, SEQ ID NO: 691.
 XX Human: full length cDNA; cDNA synthesis; oligo-capping; sa.
 KW Homo sapiens.
 OS Homo sapiens.
 PN EPI30094-AZ.
 PD 05-SEP-2001.
 PP 07-JUL-2000; 2000EP-0114089.
 XX 08-JUL-1993; 93AP-0194486.
 PR 11-JAN-2000; 2000JP-0118774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX (HELI-) HELIX RES INST.
 XX Cht 1, Nishitawa T, Isegaki T, Hayashi K, Ishii S, Kawai Y;
 P1 Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI: 2001-524255/58.
 DR 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX Claim 2: SEQ ID NO 691; 1380bp + sequence listing: English.

PS Claim 1: SEQ ID NO 23; 980bp; English.

XX The invention relates to isolated nucleic acid molecules and their
 CC encoding a novel secreted protein. The nucleic acids and proteins are used to
 CC enhance, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
 CC are also used in diagnosing a pathological condition or susceptibility
 CC to a pathological condition. Antisense to the present nucleic acids
 CC be used in alleviating symptoms associated with the disorders and in
 CC diagnostic immunoassays, e.g. enzyme immunoassays or enzyme linked
 CC immunosorbent assays (ELISA). Disorders which are diagnosed or treated
 CC include autoimmune diseases e.g. rheumatoid arthritis,
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischemia, angiogenesis, nervous system diseases and fungi
 CC Alzheimer's disease. Infections caused by bacteria and many other
 CC and cellular disorders e.g. colitis. The polypeptides can also
 CC disorder related wound healing and epithelial cell proliferation, to
 CC prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used
 CC as a food additive or preservative to increase oxidative vitamins
 CC capabilities, fat content, lipid, protein, amino acids, minerals,
 CC minerals, cofactors and other nutritional components. The present

CC sequence encodes a novel secreted protein of the invention.
 Query Match 73.6%; Score 16.2; DB 22; Length 780;
 Best Local Similarity 85.7%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 0Y 2 aagcgctgtagccgggggctc 22
 |||||||
 Db 129 aagcgctgtagccgggggctc 149

RESULT 8

AAH05059
 ID AAH05059 standard: cDNA; 786 BP.
 AC AAH05059;
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA clone (5'-primer) SEQ ID NO:1894.
 XX
 XX Human: primer: detection; diagnosis; antisense therapy; gene therapy; ss.
 XX Homo sapiens.
 XX EP1074617-A2.
 XX
 XX 07-FEB-2001.
 XX
 XX 28-JUL-2000; 2000EP-0116126.
 XX
 XX 29-JUL-1999; 99JP-0248036.
 XX 27-AUG-1999; 99JP-0300253.
 XX 11-JAN-2000; 2000JP-0118776.
 XX 02-MAY-2000; 2000JP-0183767.
 XX 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELI-) HELIX RES INST.
 XX
 XX Oda T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI: 2001-318749/34.
 XX
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 XX full-length cDNAs defined in the specification, and for the detection
 XX and/or diagnosis of the abnormality of the proteins encoded by the
 XX full-length cDNAs -
 XX
 XX Claim 1: SEQ ID 1894; 2537bp + CD ROM; English.
 XX
 XX The present invention describes primer sets for synthesizing 5602
 XX full-length cDNAs defined in the specification. Where a primer set
 XX comprises: (a) an oligo-of-primer and an oligonucleotide complementary
 XX to the complementary strand of a polynucleotide sequence, where the
 XX 5602 nucleotide sequence is defined in the specification, where the
 XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 XX of an oligonucleotide comprising a sequence complementary to a
 XX complementary strand of a polynucleotide which comprises a 5'-end
 XX polynucleotide comprising at least 15 nucleotides and a sequence
 XX complementary to a polynucleotide which comprises a 3'-end
 XX sequence and a sequence, where the combination of the
 XX oligonucleotide comprises at least 15 nucleotides and the
 XX 5'-end sequence/3'-end sequence is selected from those defined in
 XX the specification. The primer sets are useful for synthesizing
 XX polynucleotides, particularly full-length cDNAs. The primers are also useful for the
 XX detection and/or diagnosis of the abnormality of the proteins encoded by
 XX the full-length cDNAs. The primers allow obtaining of the full-length
 XX cDNAs easily without any specialized methods. AAH03166 to AAH13628 and
 XX AAH13633 to AAH18742 represent human cDNA sequences; AAH03166 to
 XX AAH09893 represent human amino acid sequences; AAH13629 to AAH13632
 XX represent oligonucleotides, all of which are used in the exemplification
 XX of the present invention.
 XX
 XX Sequence 786 BP; 136 A; 248 C; 255 G; 144 T; 3 other;
 XX
 XX Query Match 73.6%; Score 16.2; DB 22; Length 786;
 XX Best Local Similarity 85.7%; Pred. No. 5.9e+02;
 XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 2 aagcgctagcgccggggggtc 22
 XX ||||||||| |||||
 XX Db 125 aagcgctagcgccggggggtc 145

RESULT 9
 AAH05438
 ID AAH05438 standard: cDNA; 804 BP.
 AC AAH05438;
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA clone (5'-primer) SEQ ID NO:2273.
 XX
 XX Human: primer: detection; diagnosis; antisense therapy; gene therapy; ss.
 XX Homo sapiens.
 XX EP1074617-A2.
 XX
 XX 07-FEB-2001.
 XX
 XX 28-JUL-2000; 2000EP-0116126.
 XX
 XX 29-JUL-1999; 99JP-0248036.
 XX 27-AUG-1999; 99JP-0300253.
 XX 11-JAN-2000; 2000JP-0118776.
 XX 02-MAY-2000; 2000JP-0183767.
 XX 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELI-) HELIX RES INST.
 XX
 XX Oda T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI: 2001-318749/34.
 XX
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 XX full-length cDNAs defined in the specification, and for the detection
 XX and/or diagnosis of the abnormality of the proteins encoded by the
 XX full-length cDNAs -
 XX
 XX Claim 1: SEQ ID 2273; 2537bp + CD ROM; English.
 XX
 XX The present invention describes primer sets for synthesizing 5602
 XX full-length cDNAs defined in the specification. Where a primer set
 XX comprises: (a) an oligo-of-primer and an oligonucleotide complementary
 XX to the complementary strand of a polynucleotide sequence, where the
 XX 5602 nucleotide sequence is defined in the specification, where the
 XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 XX of an oligonucleotide comprising a sequence complementary to the
 XX complementary strand of a polynucleotide which comprises a 5'-end
 XX sequence and a sequence, where the combination of the
 XX oligonucleotide comprises at least 15 nucleotides and the
 XX 5'-end sequence/3'-end sequence is selected from those defined in
 XX the specification. The primer sets are useful for synthesizing
 XX polynucleotides, particularly full-length cDNAs. The primers are also useful for the
 XX detection and/or diagnosis of the abnormality of the proteins encoded by
 XX the full-length cDNAs. The primers allow obtaining of the full-length
 XX cDNAs easily without any specialized methods. AAH03166 to AAH13628 and
 XX AAH13633 to AAH18742 represent human cDNA sequences; AAH03166 to
 XX AAH09893 represent human amino acid sequences; AAH13629 to AAH13632
 XX represent oligonucleotides, all of which are used in the exemplification
 XX of the present invention.
 XX
 XX Sequence 804 BP; 168 A; 246 C; 217 G; 169 T; 4 other;
 XX
 XX Query Match 73.6%; Score 16.2; DB 22; Length 804;
 XX Best Local Similarity 85.7%; Pred. No. 5.9e+02;
 XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 2 aagcgctagcgccggggggtc 22
 XX ||||||||| |||||

DB 1129 AACGGCGTAAAGCCAGGCTTC 1109

RESULT 12

AAH15691 ID AAH15691 standard; cDNA: 1768 BP.

AAH15691:

26-JUN-2001 (first entry)

Human cDNA sequence SEQ ID NO:14600.

Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.

Homo sapiens.

EP1074617-A2.

07-FEB-2001.

28-JUL-2000: 2000EP-0116126.

29-JUL-1999: 98JP-0248036.

27-AUG-1999: 98JP-0248036.

11-JAN-2000: 2000JP-0118776.

02-MAY-2000: 2000JP-0183767.

09-JUN-2000: 2000JP-0241899.

(HELI-1) HELIX RES INST.

Ota T, Isegawa T, Mitsuoka T, Hayashi K, Saito K, Yamamoto J; Ishii S, Sugiyama T, Nakamatsu K, Nagai K, Otsuki T; WPI: 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 and/or length cDNAs defined in the specification, and for the detection full-length cDNAs.

Claim 8: SEQ ID 14060: 2537bp + CD ROW; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set (a) an oligo-of-primer and an oligonucleotide complementary to the complementary sequence of the polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is useful for antisense therapy in the gene therapy. The primer sets are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without the primers. AAH03166 to AAH15628 and AAH15633 to AAH18742 represent human cDNA. AAH15629 to AAH15632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence 1768 BP; 351 A; 487 C; 571 G; 359 T; 0 other;

Query Match 73.6%; Score 16.2; DB 22; Length 1768; Best Local Similarity 85.7%; Pred. No. 5.5e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 aagcggcgttaagccgaggtc 22
||||||| |||||
DB 125 aagcggcgttaagccgaggtc 145

RESULT 13

ABA90358/2 ID ABA90358 standard; cDNA: 1782 BP.

ABA90358:

12-FEB-2002 (first entry)

Human polynucleotide #33.

Human; nocitropic; neuroprotective; anticonvulsant; antidepressant; neuroleptic; tranquilizer; antirhythmic; cardiant; antisthmatic; antilemmatoly; antileptic; hepatotropic; virucide; antidiabetic; nephrotoxic; anorectic; cytosstatic; vaccine; neurological disease; cardiovascular disease; respiratory disease; liver disease; placental disease; cephalic cancer; male fertility; pancreatic disease; ss.

Homo sapiens.

WO200101363-A1.

01-NOV-2001.

26-APR-2001: 2001WO-US13360.

27-APR-2000: 2000US-199636P.

11-MAY-2000: 2000US-20336P.

26-MAY-2000: 2000US-20708P.

26-MAY-2000: 2000US-207346P.

(SMK) SMITHKLINE BEECHAM CORP.

(SMK) SMITHKLINE BEECHAM PLC.

Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kadnick KS; Lai Y, Xie Q;

WPI: 2002-041392/05.

P-PSDB; ABB53293.

Novel polypeptides and polynucleotides useful as a vaccine for preventing and treating diseases associated the polypeptide, e.g. Alzheimer's disease, dyallipidemia, obesity, diabetes, infertility, asthma, amnesia -

Claim 2: Page 62-63; 11sep; English.

The invention relates to an isolated polypeptide comprising a 277, 480, 581, 628, 424, 638, 229, 310, 841, 241, 359, 382, 185, 586, 1056, 744, 252, 629, 394, 471, 485, 286, 533, 495, 619, 490, 452, 255, 583, 373, 671, 810, 686 or 156 amino acid sequence as given in the specification. The polypeptides are useful for treating diseases such as neurological and psychiatric diseases including Alzheimer's, paraneuronal palsy, Huntington's disease, myotonic dystrophy, anorexia and depression; cardiovascular diseases including congestive heart failure, Hodgkin's disease and myocardial infarction; viral diseases including hypercholesterolemia, diabetes, pulmonary disease, cystic fibrosis including asthma, chronic obstructive pulmonary disease, viral diseases including hypercholesterolemia, glucose tolerance; renal disease including renal failure, acute tubular necrosis and glomerulonephritis; skeletal muscle diseases including Battenburg's disease, hypophosphatemia and obesity; gastrointestinal diseases including myotonia congenita and obesity; gastrointestinal diseases including lymphoproliferative diseases of placenta including

Query Match 73.6%; Score 16.2; DB 22; Length 1993;
 Best Local Similarity 85.7%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy . 2 aagcgagctagcgccggggtc 22
 |||||
 Db 66 aagcgagctagcgccggggtc 86
 |||||

Search completed: June 23, 2002, 15:01:16
 Job time: 81208 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleate - nucleate search, using sw model

Run on: June 23, 2002, 15:09:16 ; Search time 167.81 Seconds
(without alignments)

32.203 Million cell updates/sec

US-09-747-514a-4

1 gaagcgcgtagcgccggggggtc 22

IDENTITY: NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, NA.*
1: /cgn2.6/pctdata/1/lna/5A_COMB.seq.*
2: /cgn2.6/pctdata/1/lna/5B_COMB.seq.*
3: /cgn2.6/pctdata/1/lna/6A_COMB.seq.*
4: /cgn2.6/pctdata/1/lna/6B_COMB.seq.*
5: /cgn2.6/pctdata/1/lna/PCBUS_COMB.seq.*
6: /cgn2.6/pctdata/1/lna/bacclifl1st.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.2	78.2	7741	US-09-426-998-4	Sequence 4, Appl
C 2	15.8	78.2	5822	US-08-899-595-4	Sequence 4, Appl
C 3	15.8	71.8	5822	US-08-899-595-5	Sequence 5, Appl
C 4	15.6	70.9	942	US-08-737-412-1	Sequence 1, Appl
C 5	15.6	70.9	2126	US-08-788-354-1	Sequence 1, Appl
C 6	15.6	70.9	2126	US-08-058-725B-1	Sequence 1, Appl
C 7	15.6	70.9	2126	US-08-232-857-3	Sequence 1, Appl
C 8	15.6	70.9	2126	US-08-872-757-3	Sequence 3, Appl
C 9	15.6	70.9	3546	US-08-872-757-3	Sequence 3, Appl
C 10	15.2	69.1	1247	PCT-US91-02766-19	Sequence 19, Appl
C 11	15.2	69.1	1247	PCT-US91-02766-19	Sequence 19, Appl
C 12	15.2	69.1	1316	PCY-0891-02766-21	Sequence 21, Appl
C 13	15.2	69.1	1316	PCY-0891-02766-21	Sequence 21, Appl
C 14	15.2	69.1	1316	PCY-0891-02766-21	Sequence 21, Appl
C 15	15.2	69.1	4378	US-09-124-238A-3	Sequence 3, Appl
C 16	15.2	69.1	4378	US-09-124-238A-3	Sequence 3, Appl
C 17	15.2	69.1	6854	US-08-899-595-2	Sequence 2, Appl
C 18	15.2	69.1	6854	US-08-899-595-2	Sequence 2, Appl
C 19	15.2	69.1	12412	US-08-390-876-18	Sequence 18, Appl
C 20	15.2	69.1	22108	US-08-053-197A-3	Sequence 3, Appl
C 21	15.2	69.1	22108	US-08-053-197A-3	Sequence 3, Appl
C 22	14.8	67.3	1620	US-09-124-238A-3	Sequence 3, Appl
C 23	14.8	67.3	1620	US-09-124-238A-3	Sequence 3, Appl
C 24	14.8	67.3	1644	US-09-124-238A-3	Sequence 3, Appl
C 25	14.8	67.3	1644	US-09-124-238A-3	Sequence 3, Appl
C 26	14.8	67.3	1689	US-09-124-238A-3	Sequence 3, Appl
C 27	14.8	67.3	1689	US-09-124-238A-3	Sequence 3, Appl

ALIGNMENTS

28	14.8	67.3	4208	US-09-068-740A-10	Sequence 10, Appl
29	14.8	67.3	5590	US-08-882-046-1	Sequence 1, Appl
30	14.8	67.3	6464	US-08-400-159-5	Sequence 5, Appl
31	14.8	67.3	6464	US-08-611-729A-5	Sequence 5, Appl
32	14.6	66.4	63	US-08-284-391B-51	Sequence 51, Appl
33	14.6	66.4	63	US-08-218-950-51	Sequence 51, Appl
34	14.6	66.4	387	US-08-975-118-1	Sequence 1, Appl
35	14.6	66.4	387	US-08-975-118-1	Sequence 1, Appl
36	14.6	66.4	462	US-08-854-531-1	Sequence 1, Appl
37	14.6	66.4	462	US-08-854-531-1	Sequence 1, Appl
38	14.6	66.4	549	US-08-441-971-58	Sequence 58, Appl
39	14.6	66.4	549	US-08-441-971-58	Sequence 58, Appl
40	14.6	66.4	549	US-08-441-971-58	Sequence 58, Appl
41	14.6	66.4	549	US-08-441-971-58	Sequence 58, Appl
42	14.6	66.4	549	US-08-441-971-58	Sequence 58, Appl
43	14.6	66.4	549	US-08-441-971-58	Sequence 58, Appl
44	14.6	66.4	549	US-08-441-971-58	Sequence 58, Appl
45	14.6	66.4	549	US-08-441-971-58	Sequence 58, Appl

RESULT 1
US-09-426-998-4/C
; Sequence 4, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DOBAIN, ADRIENNE E.
; APPLICANT: DOBAIN, ADRIENNE E.
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHALIG T-TYPE CALCULON
; FILE REFERENCE: ORT 1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT PRIORITY NUMBER: US/93-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 4
; LENGTH: 7741
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; US-09-426-998-4
Query Match 78.2%; Score 17.2; DB 4; Length 7741;
Best Local Similarity 86.4%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Or 1 gaagcgcgtagcgccggggggtc 22
Db 147 GCACGCCGCAAGCGCGGCGT 126
RESULT 2
US-08-899-595-4
; Sequence 4, Application US/0889595
; Patent No. 611072
; GENERAL INFORMATION:
; APPLICANT: TAKAHASHI, SHU
; APPLICANT: TAKAHASHI, SHU
; TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MOA AND GENE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

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COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA: JP 8-242701
FILING DATE: 26-AUG-1996
APPLICATION NUMBER: JP 9-90170
FILING DATE: 25-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKEY NUMBER: 049441/0112
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5822 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Human
FEATURES:
NAME/KEY: CDS
LOCATION: 28..3972
US-08-899-595-4

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Query Match      71.8% Score 15.8; DB 3; Length 5822;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 4 gcgcgctagccggcggtc 22
    |||||
DB 143 gcgcgctagccggcggtc 161

RESULT
US-08-899-595-5/c
Sequence 5. Application US/0889595
Patent No. 6111072
GENERAL INFORMATION:
APPLICANT: Natunalye, Shuh
APPLICANT: Takahashi, No. 6111072uuki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
NUMBER OF SEQUENCES: INCLUDING SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-242701
FILING DATE: 26-AUG-1996
APPLICATION NUMBER: JP 9-90170
FILING DATE: 25-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKEY NUMBER: 049441/0112
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5822 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Human
US-08-899-595-5

```

```

Query Match      71.8% Score 15.8; DB 3; Length 5822;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 4 gcgcgctagccggcggtc 22
    |||||
DB 5680 gcgcgctagccggcggtc 5662

```

```

RESULT
US-08-732-412-1/c
Sequence 1. Application US/08732412
Patent No. 6017866
GENERAL INFORMATION:
APPLICANT: Able, Wolfgang
APPLICANT: Gentile, Gilbert
TITLE OF INVENTION: LIPASES WITH IMPROVED
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genzyme International, Inc.
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM Compatible
SOFTWARE: PASTISO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,412
FILING DATE: 22-OCT-1996
PRIOR APPLICATION DATA: PCT/EP95/01687
APPLICATION NUMBER: EP 9420125.5
FILING DATE: 04-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,60307-US
REFERENCE/DOCKEY NUMBER: 049441/0112
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-737-412-1

Query Match
Best Local Similarity 70.9%; Score 15.6; DB 3; Length 942;
Matches 18; Conservative 0; Pctid No. 1; 5e+02;
Mismatches 4; Indels 0; Gaps 0;

Oy 1 gaagcgagcagcgccgagcggtc 22
||||| | | | | | | | | | | | | | | | | |
Db 144 GAGCGCGAGCGCGCGCGGTGTC 123

RESULT 5

US-08-789-354-1
Sequence 1, Application US/08789354
Patent No. 5851798

GENERAL INFORMATION:
INVENTOR: BASHON, USMAN
APPLICANT: BASHON, USMAN
TITLE OF INVENTION: Cloning of Human GPR14 Re
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sallinkline Beecham Corporation
Street: 709 Wedeland Road
City: King of Prussia
State: PA
Country: USA
ZIP: 19406
COMPUTER READABLE FORM:
COMPUTER TYPE: Diskette
COMPUTER SYSTEM: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,354
FILING DATE: 27-JAN-1997
PRIORITY DATE: 435
PRIORITY APPLICATION:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: P50610
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-789-354-1

Query Match
Best Local Similarity 70.9%; Score 15.6; DB 2; Length 2126;
Matches 18; Conservative 0; Pctid No. 1; 5e+02;
Mismatches 4; Indels 0; Gaps 0;
Oy 1 gaagcgagcagcgccgagcggtc 22
| | | | | | | | | | | | | | | | | |

Db 1694 GAGCGCGGAGAGCGCGGAGCC 1715

RESULT 6

US-09-110-937-1
Sequence 1, Application US/09110937A
Patent No. 6005074

GENERAL INFORMATION:
INVENTOR: BASHON, USMAN
APPLICANT: BASHON, USMAN
TITLE OF INVENTION: CLONING OF HUMAN GPR14 RECEPTOR
FILE REFERENCE: P50610-1
CURRENT APPLICATION NUMBER: US/09/110,937A
CURRENT FILING DATE: 1998-07-06
NUMBER OF SEQ ID NOS: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FastSeq for Windows Version 3.0
SEQ ID NO: 1
LENGTH: 2126
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-110-937-1

Query Match
Best Local Similarity 70.9%; Score 15.6; DB 3; Length 2126;
Matches 18; Conservative 0; Pctid No. 1; 5e+02;
Mismatches 4; Indels 0; Gaps 0;

Oy 1 gaagcgagcagcgccgagcggtc 22
||||| | | | | | | | | | | | | | | | | |
Db 1694 gaagcgagcgagcgcgcggtc 1715

RESULT 7

US-09-058-725B-1
Sequence 1, Application US/09058725B
Patent No. 613420

GENERAL INFORMATION:
INVENTOR: SARAU, HENRY
APPLICANT: SARAU, HENRY
APPLICANT: FOLEY, JAMES
TITLE OF INVENTION: A Method of Finding Angonist
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sallinkline Beecham Corporation
Street: 709 Wedeland Road
City: King of Prussia
State: PA
Country: USA
ZIP: 19406
COMPUTER READABLE FORM:
COMPUTER TYPE: Diskette
MEDIUM TYPE: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,725B
FILING DATE: 27-JAN-1997
PRIORITY DATE: 435
PRIORITY APPLICATION:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GP50005-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 2126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-058-725B-1

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Query Match	70.98;	Score 15.6;	DB 3;	Length 2126;
Best Local Similarity	81.88;	Pred. No. 1.5e+02;		
Matches	18: Conservative	0: Mismatches	4: Indels	0: Gaps

Qy 1 gaagcgcgtacgcccggggtc 22

RESULT 8
US-09-232-857-1
US-09232857

1
2 GENERAL INVESTIGATIVE DIVISION, STEPHEN
3 APPLICANT: DOMINGAS, STEPHEN
4 APPLICANT: WILLETTTE, ROBERT
5 APPLICANT: ALTYAR, NAMBI
6 APPLICANT: ROMANIC, ANNE
7 APPLICANT: KHANDOUDI, NASSIRAH
8 APPLICANT: GOTT, BERNARD, KASSIRAH
9 APPLICANT: AL-BANAN, KAMAL
10 APPLICANT: AL-BAHRI, ROBERT S.
11 APPLICANT: FOLEY, JAMES J.
12 APPLICANT: SARAU, HENRY
13 APPLICANT: CHAMBERS, JON K.
14 APPLICANT: SHABON, USMAN
15 APPLICANT: BEKESMA, DEK
16 TITLE OF INVENTION: A METHOD OF FINDING ACOWIST
17 TITLE OF INVENTION: AND ANTAGONIST TO HUMAN AND RAT GRIPI
18 NUMBER OF SEQUELATION: 1
19 CORRESPONDENCE ADDRESS:
20 CORRESPONDENCE: Palmer 6 Prestila
21 STREET: P. O. Box 980
22 CITY: valley Forge

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-232-857-1

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Query Match	70.9%	Score 15.6;	DB 3;	Length 2126;
Best Local Similarity	81.8%	Pred. No. 1.5e+02;		
Matches 18: Conservative		Mismatches 4;	Indels 0;	Gaps 0

QY 1 gaagcgcgtacgcgcggggtc 22

Db 1694 GCAGCGGGGAGCCGGGGCC 1715

US-08-872-757-3/c
; Sequence 3, Application US/08872757

1 GENERAL INFORMATION:
2
3 APPLICANT: PROCKOP, DAVID J.
4
5 APPLICANT: Kojima, Yoshio
6
7 APPLICANT: Saitoh, Alexander
8
9 TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
10 TITLE OF INVENTION: PROCESSES, METHODS AND USES THEREOF
11
12 NUMBER OF SEQUENCES: 6
13
14 CORRESPONDENCE ADDRESS:
15
16 ADDRESSEE: Penate & Edmonds
17
18 STREET: 1155 Avenue of the Americas
19
20 CITY: New York
21
22 STATE: New York
23
24 COUNTRY: U.S.A.
25
26 ZIP: 10036-2711
27
28 COMPUTER READABLE FORM:
29
30 MEDIUM TYPE: floppy disk
31
32 COMPUTER: IBM PC compatible
33
34 OPERATING SYSTEM: DOS/MS-DOS
35
36 RELEASED IN PATENT RELEASE 1.0. Version 1.30
37
38 CURRENT APPLICATION DATA:
39
40 FILING DATE: 05/08/87, 7/57
41
42 FILING DATE: 10-JUN-1997

Query Match	70.9%	Score 15.6	DB 4	Length 3546
Best Local Similarity	81.8%	Pred. No. 1.5e+02		
Matches 18	Conservative	0	Mismatches 4	Indels 0
				Gaps 0

Qy 1 gaagcgcgtlagcgcggggtc 22

Db 2463 GAAGCGCGGAGAGCGGGGCC 2442

```

RESULT 10
PCT-US91-02766-19/c
: Sequence 19: Application PC/7US9102766
: GENERAL INFORMATION:
: APPLICANT: NASCIMENTO, CARLOS G.
: APPLICANT: CALDERON-CACIA, MARIA D.
: TITLE OF INVENTION: GLYCOSYLATED PDGF
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESS: 545 Middlefield Road, Suite 200
: STREET: Menlo Park
: CITY: Menlo Park
: STATE: California
: COUNTRY: USA
: ZIP: 94025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/02766
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/515,474
: FILING DATE: 26-Apr-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: ROBINS, ROBERTA L.
: REGISTRATION NUMBER: 33,208
: TELEPHONE: (415) 327-7250
: TELECOMMUNICATION INFORMATION:
: TELEFAX: (415) 327-2951
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1247 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 396..983
: PCT-US91-02766-19

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Query Match 69.1%; Score 15.2; DB 5; Length 1247;
 Best Local Similarity 85.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 131 GAAGCGCGGAGAGCGGGGCC 112

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RESULT 11
5219759-3/c
: Patent No. 5219759
: INVENTOR: HENRIK, CARL; HENRIK, REINHOLD; CHRISTER, WESTERMARK,
: BENGT KNOTT TIMOTHY; CALDERON, MARIA D.; CALDERON, J.
: TITLE OF INVENTION: RECOMBINANT DNA ENCODING PDGF A-CHAIN
: POLYPEPTIDE AND EXPRESSION VECTORS
: NUMBER OF SEQUENCES: 18
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 07/574,540
: FILING DATE: 26-Apr-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 41,299
: FILING DATE: 22-Apr-1987

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: SEQ ID NO:3;
 : LENGTH: 1247
 5219759-3

Query Match 69.1%; Score 15.2; DB 6; Length 1247;
 Best Local Similarity 85.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 131 GAAGCGCGGAGAGCGGGGCC 112

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RESULT 12
PCT-US91-02766-21/c
: Sequence 21: Application PC/7US9102766
: GENERAL INFORMATION:
: APPLICANT: NASCIMENTO, CARLOS G.
: APPLICANT: CALDERON-CACIA, MARIA D.
: TITLE OF INVENTION: GLYCOSYLATED PDGF
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESS: 545 Middlefield Road, Suite 200
: STREET: Menlo Park
: CITY: Menlo Park
: STATE: California
: COUNTRY: USA
: ZIP: 94025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/02766
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/515,474
: FILING DATE: 26-Apr-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: ROBINS, ROBERTA L.
: REGISTRATION NUMBER: 33,208
: TELEPHONE: (415) 327-7250
: TELECOMMUNICATION INFORMATION:
: TELEFAX: (415) 327-2951
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1247 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 396..1028
: PCT-US91-02766-21

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Query Match 69.1%; Score 15.2; DB 5; Length 1316;
 Best Local Similarity 85.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 131 GAAGCGCGGAGAGCGGGGCC 112

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RESULT 13
5219759-1/c
: Patent No. 5219759

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APPLICANT: HELDIN, CARL-HEMIK, BETHSHOLTZ, CHRISTER:WESTERMARK,
 BENGT-KNOTT, TIMOTHY J.;SCOTT, JAMES BELL, GREGG J.
 TITLE OF INVENTION: RECOMBINANT DNA ENCODING PDGF A-CHAIN
 POLYPEPTIDE AND EXPRESSION VECTORS
 NUMBER OF SEQUENCES: 18
 CURRENT APPLICATION DATA:
 PRIORITY NUMBER: 09/07/574,540
 FILING DATE: 27-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 41,299
 FILING DATE: 22-APR-1987
 SEQ ID NO:1:
 5219759-1
 LENGTH: 1316

Query Match 69.1%; Score 15.2; DB 6; Length 1316;
 Best Local Similarity 85.0%; Pred. No. 2, 1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 aagcgcgttagccgcggg 20
 Db 131 aagcgcgttagccgcggg 112

RESULT 14
 US-09-080-897-3
 Sequence 3, Application US/09080897
 Patent No. 6855732
 GENERAL INFORMATION:
 APPLICANT: Kling, Mary-Claire
 APPLICANT: Lynch, Eric D.
 APPLICANT: Lee, Ming
 APPLICANT: Morrow, Jan E.
 APPLICANT: Welch, Piri L.
 APPLICANT: Leon, Pedro E.
 TITLE OF INVENTION: Modulators of Actin
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 75 DENISE DRIVE
 CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94010
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CHAIN: 11
 APPLICATION NUMBER: US/09/080,897
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: 09/197-001
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4378 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-080-897-3

Query Match 69.1%; Score 15.2; DB 2; Length 4378;
 Best Local Similarity 85.0%; Pred. No. 2, 1e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 3 aagcgcgttagccgcgggctc 22
 Db 52 aagcgcgttagccgcgggctc 71

RESULT 15
 US-09-323-735-3
 Sequence 3, Application US/09323735
 Patent No. 6197922
 GENERAL INFORMATION:
 APPLICANT: Kling, Mary-Claire
 APPLICANT: Lynch, Eric D.
 APPLICANT: Lee, Ming
 APPLICANT: Morrow, Jan E.
 APPLICANT: Welch, Piri L.
 APPLICANT: Leon, Pedro E.
 TITLE OF INVENTION: Modulators of Actin
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 75 DENISE DRIVE
 CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94010
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/323,735
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/080,897
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: 09/197-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4378 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-323-735-3

Query Match 69.1%; Score 15.2; DB 4; Length 4378;
 Best Local Similarity 85.0%; Pred. No. 2, 1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 3 aagcgcgttagccgcgggctc 22
 Db 52 aagcgcgttagccgcgggctc 71
 Search completed: June 23, 2002, 15:09:20
 Job Time: 78584 sec

EM 200104
ED Entered STN: 20010425
Last Updated on STN: 20010425
Entered Medline: 20010419

L11 ANSWER 5 OF 16 MEDLINE
AN 2001015399 MEDLINE
DN 20465132 PubMed ID: 11008205
TI Urokinase-type plasminogen activator and its receptor in colorectal cancer: independent prognostic factors of metastasis and cancer-specific survival and potential therapeutic targets.
AU Yang J L; Seetoo D q; Wang Y; Ranson M; Berney C R; Ham J M; Russell P J; Crowe P J
CS Department of Surgery, Faculty of Medicine of University of New South Wales, Prince of Wales Hospital, Randwick, Australia.. j.yang@unsw.edu.au
SO INTERNATIONAL JOURNAL OF CANCER, (2000 Sep 20) 89 (5) 431-9.
Journal code: 0042124. ISSN: 0020-7136.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200011
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001101

L11 ANSWER 6 OF 16 MEDLINE
AN 1999290668 MEDLINE
DN 99290668 PubMed ID: 10364000
TI Prostaglandin J2 and 15-deoxy-delta12,14-prostaglandin J2 induce proliferation of cyclooxygenase-depleted colorectal cancer cells.
AU Chinery R; Coffey R J; Graves-Deal R; Kirkland S C; Sanchez S C; Zackert W E; Oates J A; Morrow J D
CS Department of Medicine, and The Vanderbilt Cancer Center, Vanderbilt University School of Medicine, Nashville, Tennessee 37232, USA.
NC CA77839 (NCI)
DK48831 (NIDDK)
GM15431 (NIGMS)
+
SO CANCER RESEARCH, (1999 Jun 1) 59 (11) 2739-46.
Journal code: 2984705R. ISSN: 0008-5472.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199906
ED Entered STN: 19990714
Last Updated on STN: 19990714
Entered Medline: 19990629

L11 ANSWER 7 OF 16 MEDLINE
AN 93388005 MEDLINE
DN 93388005 PubMed ID: 8104163
TI UICC/CRC conference on targeted cancer therapy. Royal Free Hospital School of Medicine, London, December 17-19, 1991.
AU Begent R H
SO INTERNATIONAL JOURNAL OF CANCER, (1993 Sep 30) 55 (3) 355-8.
Journal code: 0042124. ISSN: 0020-7136.
CY United States
DT Conference; Conference Article; (CONGRESSES)
LA English
FS Priority Journals
EM 199310
ED Entered STN: 19931105

Last Updated on STN: 19990129
Entered Medline: 19931021

L11 ANSWER 8 OF 16 MEDLINE
AN 93285101 MEDLINE
DN 93285101 PubMed ID: 8389694
TI Linkage of superantigen-like stimulation of syngeneic T cells in a mouse model of follicular center B cell lymphoma to transcription of endogenous mammary tumor virus.
AU Tsiagbe V K; Yoshimoto T; Asakawa J; Cho S Y; Meruelo D; Thorbecke G J
CS Department of Pathology, Kaplan Comprehensive Cancer Center, New York University School of Medicine, NY 10016.
NC CA-14462 (NCI)
CA-22247 (NCI)
CA-31346 (NCI)
SO EMBO JOURNAL, (1993 Jun) 12 (6) 2313-20.
Journal code: 8208664. ISSN: 0261-4189.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L11933
EM 199307
ED Entered STN: 19930723
Last Updated on STN: 19970203
Entered Medline: 19930715

L11 ANSWER 9 OF 16 MEDLINE
AN 93171257 MEDLINE
DN 93171257 PubMed ID: 8382205
TI Inositol 1,4,5-trisphosphate receptor expression in cardiac myocytes.
AU Moschella M C; Marks A R
CS Department of Medicine, Mount Sinai School of Medicine, New York 10029.
SO JOURNAL OF CELL BIOLOGY, (1993 Mar) 120 (5) 1137-46.
Journal code: 0375356. ISSN: 0021-9525.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199303
ED Entered STN: 19930402
Last Updated on STN: 19980206
Entered Medline: 19930323

L11 ANSWER 10 OF 16 CAPLUS COPYRIGHT 2002 ACS
AN 2001:833564 CAPLUS
DN 135:367649
TI Identification of sequence motifs in oligonucleotides with antisense activity by correlation analysis
IN Freier, Susan M.; Matveeva, Olga; Tsodikov, Alexander; Giddings, Michael C.; Wyatt, Jacqueline R.
PA Isis Pharmaceuticals, Inc., USA; University of Utah Research Foundation
SO PCT Int. Appl., 57 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 2001085996	A1	20011115	WO 2001-US14157	20010502
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RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ,
 VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
 DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
 BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 2000-568165 A 20000509
 RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 11 OF 16 CAPLUS COPYRIGHT 2002 ACS
 AN 2000:772742 CAPLUS
 DN 133:330554
 TI Protein and cDNA sequences of corn NPR1 gene and uses thereof in plant
 disease control
 IN Crane, Edmund H., III; Rice, Douglas A.; Simmons, Carl R.; Tossberg, John
 T.; Sandahl, Gary A.; Zhang, Lingyu
 PA Pioneer Hi-Bred International, Inc., USA
 SO PCT Int. Appl., 86 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000065037	A2	20001102	WO 2000-US10479	20000419
	WO 2000065037	A3	20010726		
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	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	EP 1173575	A2	20020123	EP 2000-928204	20000419
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
	BR 2000009980	A	20020409	BR 2000-9980	20000419
PRAI US 1999-130692P	P		19990423		
	WO 2000-US10479	W	20000419		

L11 ANSWER 12 OF 16 CAPLUS COPYRIGHT 2002 ACS
 AN 2000:751508 CAPLUS
 DN 134:205764
 TI Urokinase-type plasminogen activator and its receptor in colorectal
 cancer: independent prognostic factors of metastasis and cancer-specific
 survival and potential therapeutic targets
 AU Yang, Jia-Lin; Seetoo, Da-qiang; Wang, Yao; Ranson, Marie; Berney,
 Christophe R.; Ham, John M.; Russell, Pamela J.; Crowe, Philip J.
 CS Department of Surgery, Faculty of Medicine of University of New South
 Wales, Randwick, Australia
 SO International Journal of Cancer (2000), 89(5), 431-439
 CODEN: IJCNW; ISSN: 0020-7136
 PB Wiley-Liss, Inc.
 DT Journal
 LA English
 RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 13 OF 16 CAPLUS COPYRIGHT 2002 ACS
 AN 1999:405087 CAPLUS
 DN 131:57413
 TI Protein 14-3-3.sigma. arrest of the cell cycle provides the basis for

diagnostic assays and therapeutic compositions
 IN Hermeking, Heiko; Vogelstein, Bert; Kinzler, Kenneth W.
 PA The Johns Hopkins Univ., USA
 SO PCT Int. Appl., 73 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9931240	A2	19990624	WO 1998-US26924	19981218
	WO 9931240	A3	19990902		
	W:		AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM		
	RW:		GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG		
	US 6335156	B1	20020101	US 1998-210748	19981215
	CA 2315279	AA	19990624	CA 1998-2315279	19981218
	AU 9918314	A1	19990705	AU 1999-18314	19981218
	AU 744193	B2	20020221		
	EP 1037987	A2	20000927	EP 1998-963256	19981218
	R:		AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI		
PRAI	US 1997-69416P	P	19971218		
	US 1998-210748	A	19981215		
	WO 1998-US26924	W	19981218		

L11 ANSWER 14 OF 16 CAPLUS COPYRIGHT 2002 ACS
 AN 1999:368555 CAPLUS
 DN 131:125831
 TI Prostaglandin J2 and 15-deoxy-.DELTA.12,14-prostaglandin J2 induce proliferation of cyclooxygenase-depleted colorectal cancer cells
 AU Chinery, Rebecca; Coffey, Robert J.; Graves-Deal, Ramona; Kirkland, Susan C.; Sanchez, Stephanie C.; Zackert, William E.; Oates, John A.; Morrow, Jason D.
 CS Departments of Medicine and Cell Biology and The Vanderbilt Cancer Center, Vanderbilt University School of Medicine, Nashville, TN, 37232, USA
 SO Cancer Research (1999), 59(11), 2739-2746
 CODEN: CNREA8; ISSN: 0008-5472
 PB AACR Subscription Office
 DT Journal
 LA English
 RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 15 OF 16 CAPLUS COPYRIGHT 2002 ACS
 AN 1999:92323 CAPLUS
 TI Hydrolysis of GpppG, a model for the 5'-cap of mRNA by dinuclear metal ion complexes
 AU Morrow, Janet R.; McCue, Kevin P.
 CS Department of Chemistry, State University of New York, Amherst, NY, 14260-3000, USA
 SO Book of Abstracts, 217th ACS National Meeting, Anaheim, Calif., March 21-25 (1999), INOR-506 Publisher: American Chemical Society, Washington, D. C.
 CODEN: 67GHA6
 DT Conference; Meeting Abstract
 LA English

L11 ANSWER 16 OF 16 CAPLUS COPYRIGHT 2002 ACS
AN 1993:536993 CAPLUS
DN 119:136993
TI Linkage of superantigen-like stimulation of syngeneic T cells in a mouse
model of follicular center B cell lymphoma to transcription of endogenous
mammary tumor virus
AU Tsiagbe, V. K.; Yoshimoto, T.; Asakawa, J.; Cho, S. Y.; Meruelo, D.;
Thorbecke, G. J.
CS Sch. Med., New York Univ., New York, NY, 10016, USA
SO EMBO J. (1993), 12(6), 2313-20
CODEN: EMJODG; ISSN: 0261-4189
DT Journal
LA English

=> d his

(FILE 'HOME' ENTERED AT 15:54:14 ON 25 JUN 2002)

FILE 'BIOSIS, MEDLINE, CAPLUS' ENTERED AT 15:55:44 ON 25 JUN 2002

L1	183033 PSEUDOMONAS
L2	78120 VIRULENCE
L3	3966 L1 AND L2
L4	2 L3 AND CRC
L5	93 CATABOLITE (W) REPRESSION (W) CONTROL
L6	1 L1 AND L2 AND L5
L7	4292 CRC
L8	2 L3 AND L7
L9	58738 ANTISENS?
L10	11697 RIBOZYM?
L11	16 L7 AND L9
L12	0 L7 AND L10

